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- (54) **METHOD FOR INHIBITING BONE RESORPTION**
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None
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ABSTRACT

The invention is directed to a method of inhibiting bone resorption. The method comprises administering to a human an amount of sclerostin inhibitor that reduces a bone resorption marker level for at least 2 weeks. The invention also provides a method of monitoring anti-sclerostin therapy comprising measuring one or more bone resorption marker levels, administering a sclerostin binding agent, then measuring the bone resorption marker levels. Also provided is a method of increasing bone mineral density; a method of ameliorating the effects of an osteoclast-related disorder; a method of treating a bone-related disorder by maintaining bone density; and a method of treating a bone-related disorder in a human suffering from or at risk of hypocalcemia or hypercalcemia, a human in which treatment with a parathyroid hormone or analog thereof is contraindicated, or a human in which treatment with a bisphosphonate is contraindicated.

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FIGURE 1

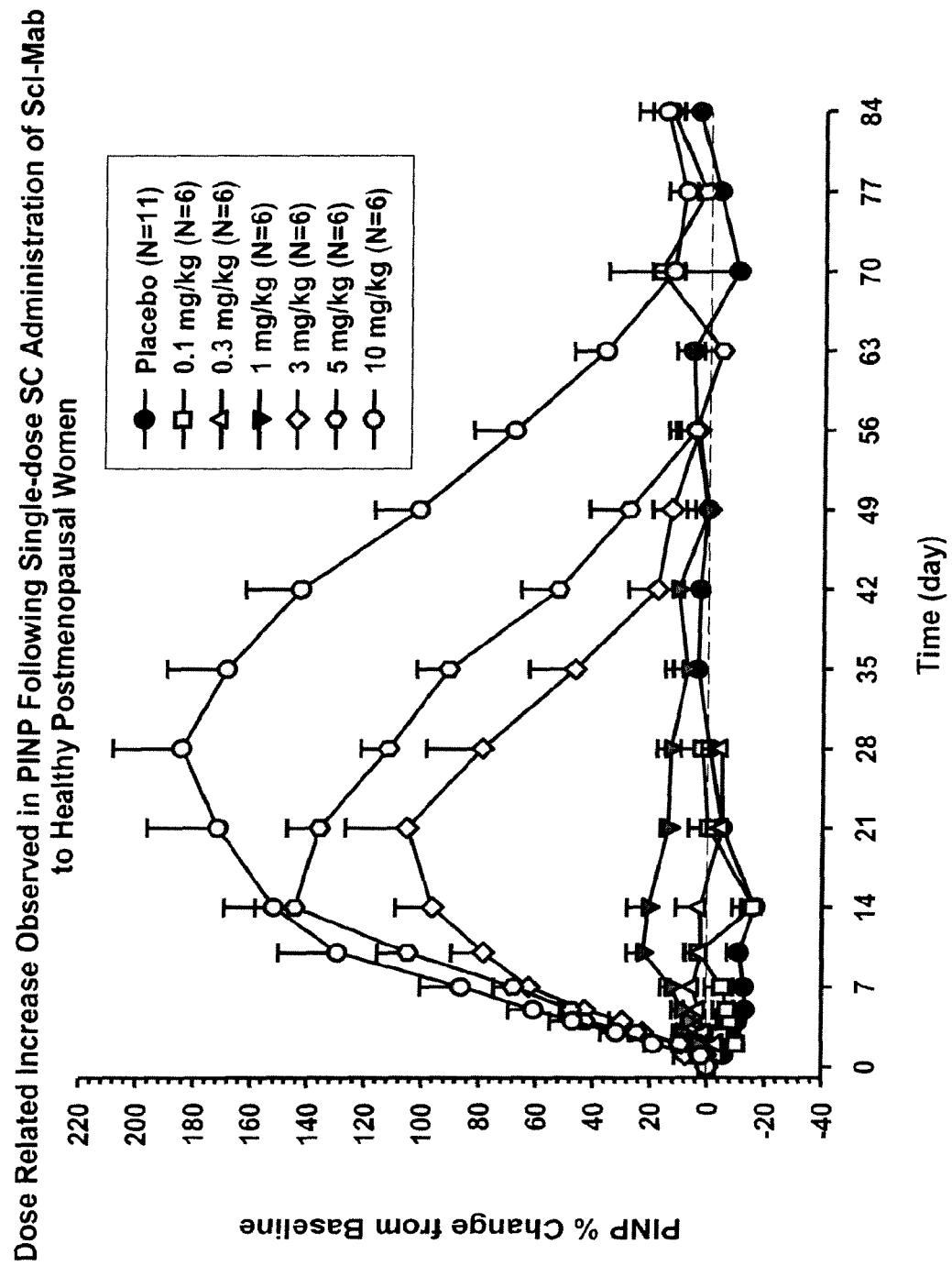


FIGURE 2
Dose Related Increase Observed in BSAP Following Single-dose SC Administration of Scl-Mab to Healthy Postmenopausal Women

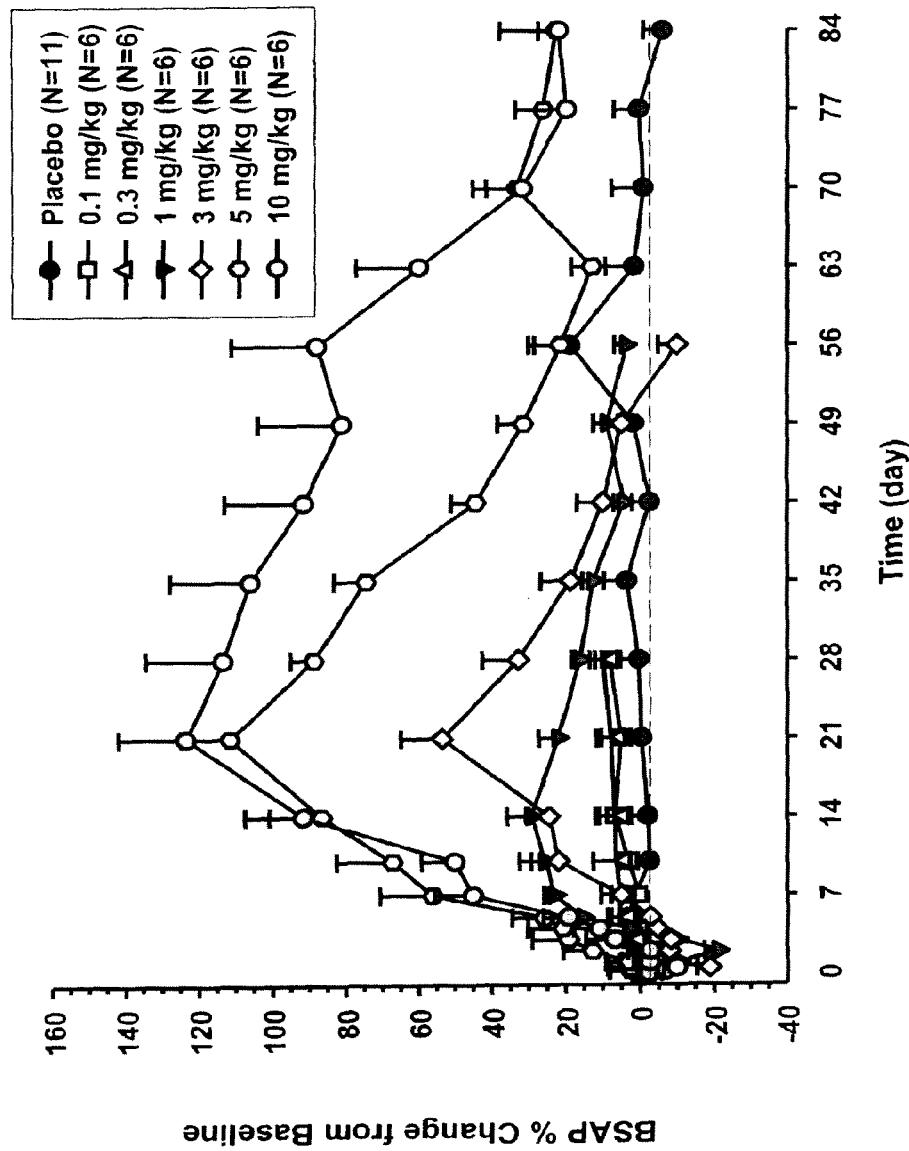


FIGURE 3

Dose Related Increase Observed in Osteocalcin Following Single-dose SC Administration of Scl-Mab to Healthy Postmenopausal Women

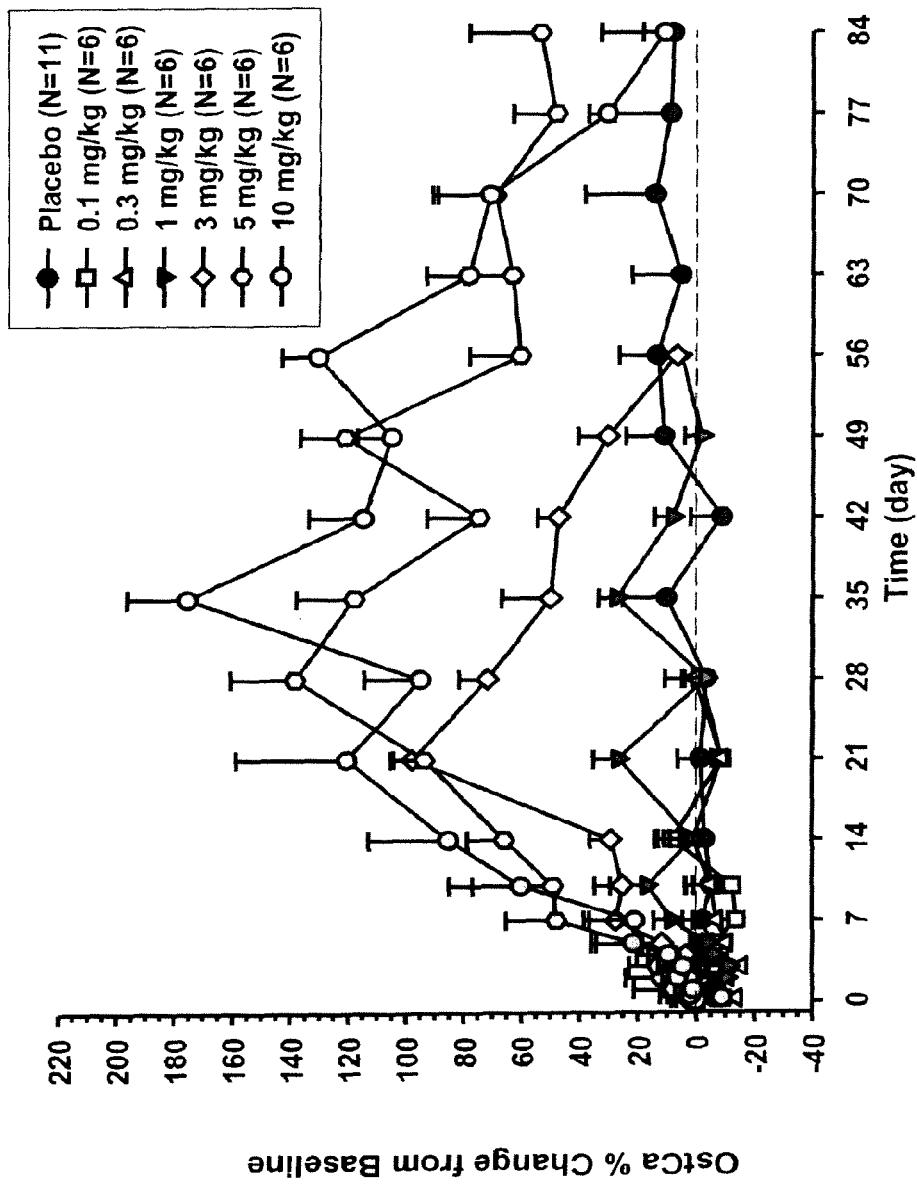


FIGURE 4

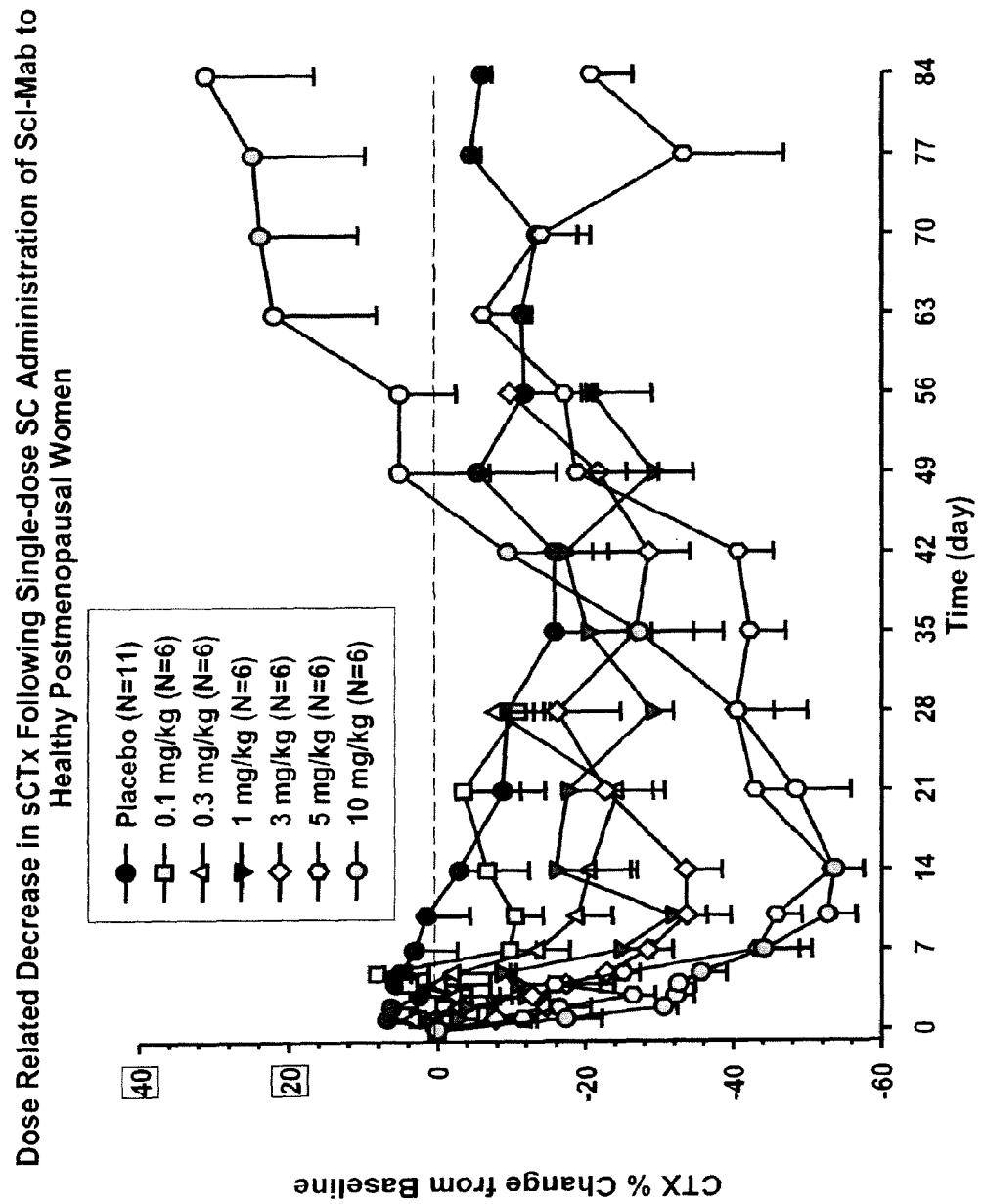


FIGURE 5

Large Anabolic Window Following Single SC Doses of 5 & 10 mg/kg Scl-Mab to Healthy Postmenopausal Women

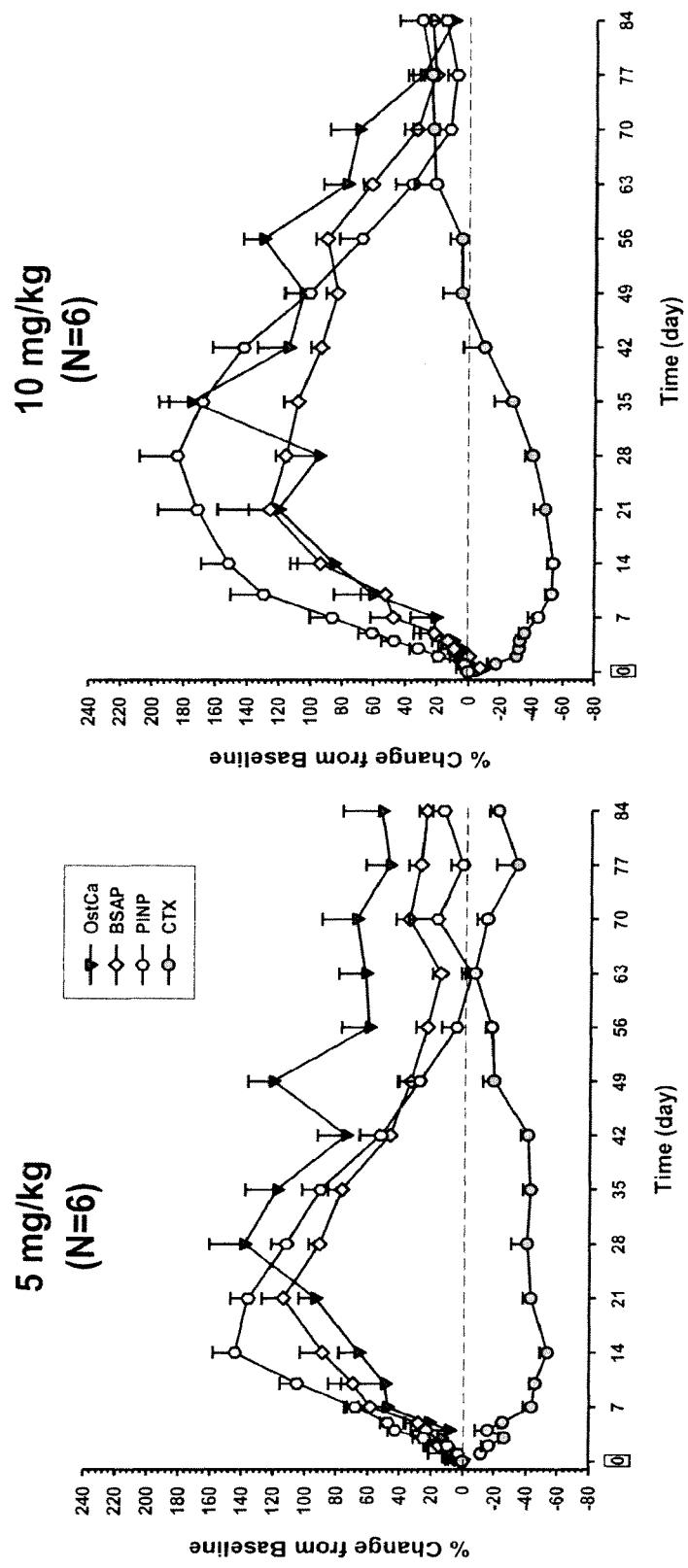


FIGURE 6

No Clinically Significant Changes in Serum Calcium Following Single-dose SC Administration of Sci-Mab to Healthy Postmenopausal Women

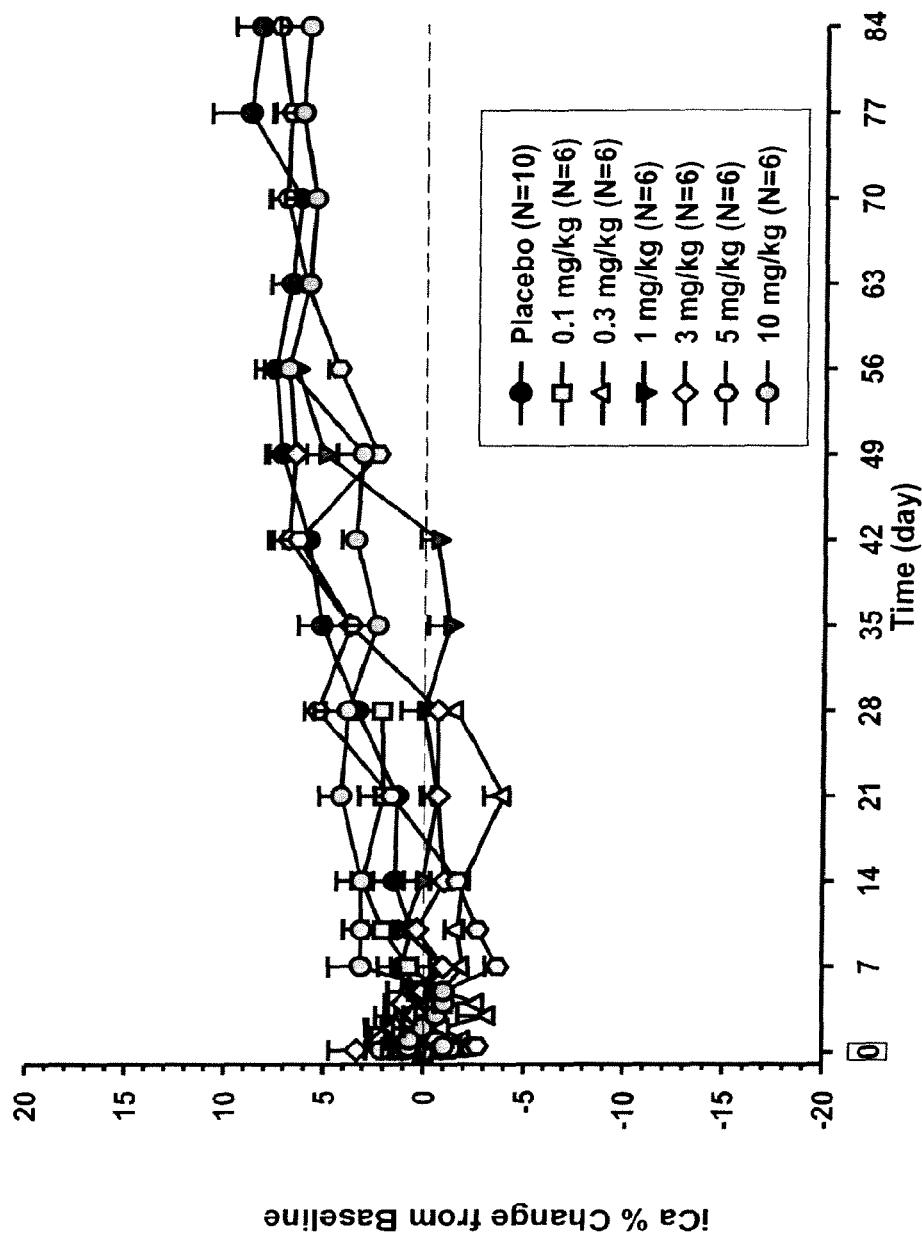
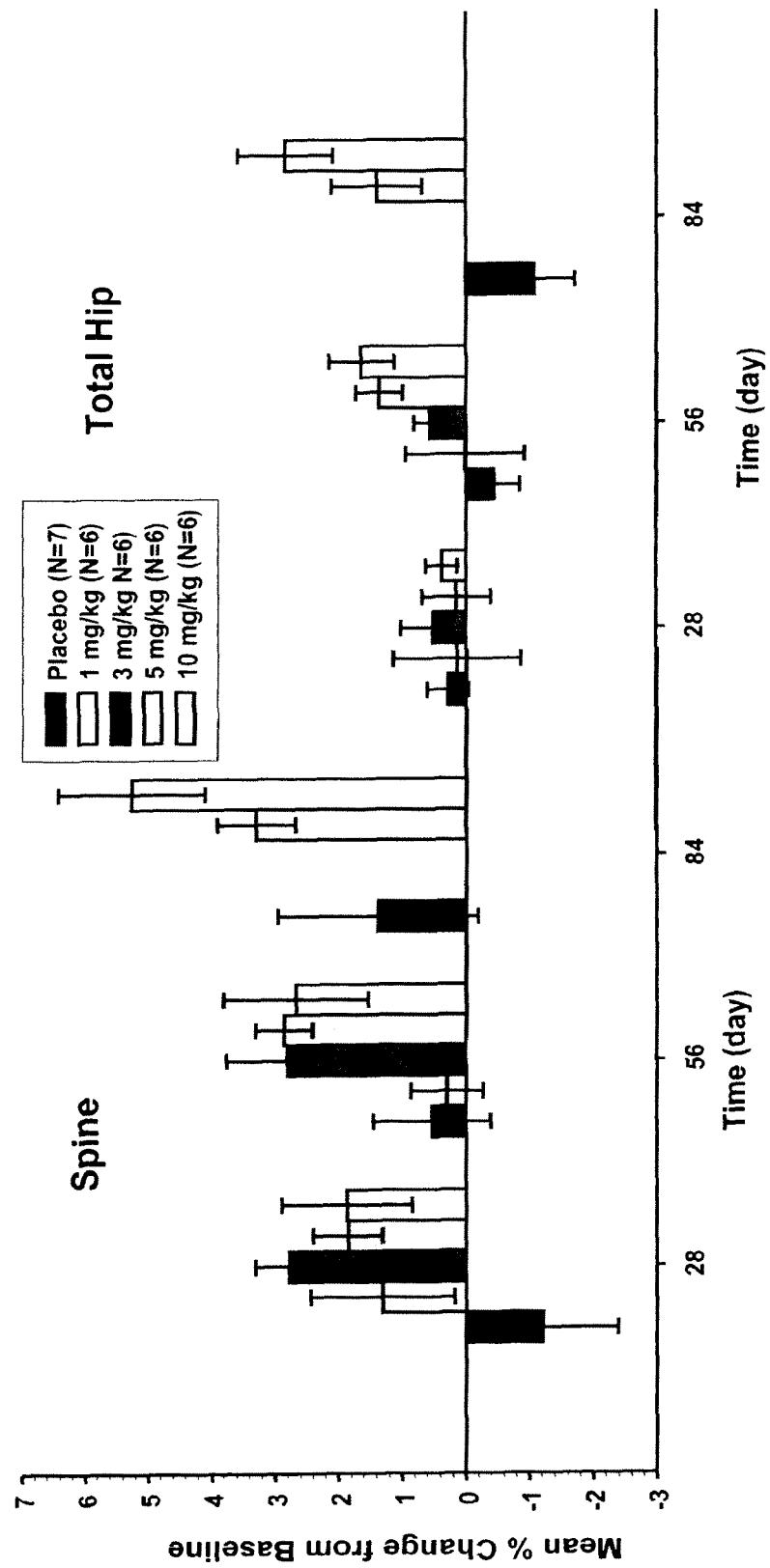


FIGURE 7
Single Doses of Scl-Mab Resulted in an Increase in BMD in Healthy Postmenopausal Women



1
**METHOD FOR INHIBITING BONE
RESORPTION**

**CROSS-REFERENCE TO RELATED
APPLICATIONS AND INCORPORATION BY
REFERENCE**

This application is continuation of U.S. patent application Ser. No. 13/090,075 (now U.S. Pat. No. 8,440,193), filed Apr. 19, 2011, which is a divisional of U.S. patent application Ser. No. 12/212,327 (now U.S. Pat. No. 8,017,120), filed Sep. 17, 2008, which in turn claims priority to U.S. Provisional Patent Application No. 60/973,024 filed Sep. 17, 2007.

The following applications are hereby incorporated by reference in their entirety: U.S. patent application Ser. No. 11/410,540 (now U.S. Pat. No. 8,033,108), filed Apr. 25, 2006, which claims priority to U.S. Provisional Patent Application No. 60/792,645, filed Apr. 17, 2006, U.S. Provisional Patent Application No. 60/782,244, filed Mar. 13, 2006, U.S. Provisional Patent Application No. 60/776,847, filed Feb. 24, 2006, and U.S. Provisional Patent Application No. 60/677,583, filed May 3, 2005; and U.S. patent application Ser. No. 11/411,003 (issued as U.S. Pat. No. 7,592,429), filed Apr. 25, 2006, which claims priority to U.S. Provisional Patent Application No. 60/792,645, filed Apr. 17, 2006, U.S. Provisional Patent Application No. 60/782,244, filed Mar. 13, 2006, U.S. Provisional Patent Application No. 60/776,847, filed Feb. 24, 2006, and U.S. Provisional Patent Application No. 60/677,583, filed May 3, 2005.

**INCORPORATION BY REFERENCE OF
MATERIAL SUBMITTED ELECTRONICALLY**

Incorporated by reference in its entirety is a computer-readable nucleotide/amino acid sequence listing submitted concurrently herewith and identified as follows: ASCII (text) file named “43242D_SubSeqListing.txt,” 507,468 bytes, created on Jul. 8, 2013.

TECHNICAL FIELD OF THE INVENTION

The invention generally relates to methods of using sclerostin binding agents to modulate bone density.

BACKGROUND OF THE INVENTION

Loss of bone mineral content can be caused by a wide variety of conditions and may result in significant medical problems. For example, osteoporosis is a debilitating disease in humans and is characterized by marked decreases in skeletal bone mass and mineral density, structural deterioration of bone, including degradation of bone microarchitecture and corresponding increases in bone fragility (i.e., decreases in bone strength), and susceptibility to fracture in afflicted individuals. Osteoporosis in humans is generally preceded by clinical osteopenia, a condition found in approximately 25 million people in the United States. Another 7-8 million patients in the United States have been diagnosed with clinical osteoporosis. The frequency of osteoporosis in the human population increases with age. Among Caucasians, osteoporosis is predominant in women who, in the United States, comprise 80% of the osteoporosis patient pool. The increased fragility and susceptibility to fracture of skeletal bone in the aged is aggravated by the greater risk of accidental falls in this population. Fractured hips, wrists, and vertebrae are among the most common injuries associated with osteoporosis. Hip fractures in particular are extremely

uncomfortable and expensive for the patient, and for women, correlate with high rates of mortality and morbidity.

SUMMARY OF THE INVENTION

The invention is directed to methods of using a sclerostin inhibitor for inhibiting bone resorption in humans. The method comprises administering to a human an amount of sclerostin inhibitor that is effective to reduce the level of a marker of bone resorption and optionally increase the level of a marker of bone formation. In some embodiments, bone resorption is inhibited and bone formation is increased for at least about 7 days, 2 weeks, 3 weeks, 4 weeks, 1 month, 5 weeks, 6 weeks, 7 weeks, 8 weeks, 2 months, 3 months or longer. In related embodiments, the invention provides a method of increasing bone mineral density or treating a bone-related disorder. The invention further provides a method of ameliorating the effects of an osteoclast-related disorder. The method comprises administering to a human a sclerostin inhibitor that reduces the level of a marker of bone resorption compared to bone marker levels absent treatment. The sclerostin inhibitor also increases the level of a marker of bone formation by at least about 10% compared to bone marker levels absent treatment. The sclerostin inhibitor can be administered via a single dose or in multiple doses. For example, the sclerostin inhibitor can be administered in a short-term therapy regimen to, e.g., increase bone formation, and/or can be administered long-term to prevent loss of bone mineral density in a maintenance therapeutic regimen.

In any of the methods disclosed herein, the level of one or more markers of bone resorption is reduced by at least about 5%, 10%, 15%, 20%, 30%, 40%, 50% or more for at least 2 weeks, 3 weeks, 30 days, 1 month, 6 weeks, 2 months or longer, compared to pre-treatment levels or normal levels for that patient population. By way of non-limiting example, the level of the marker of bone resorption by 3 weeks after treatment is decreased by, e.g., at least about 20% compared to pre-treatment levels or normal levels for that patient population. In any of the preceding methods, the level of the marker of bone formation is increased by at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, about 100% or more for at least about 2 weeks, 3 weeks, 30 days, 1 month, 6 weeks, 2 months or longer, compared to pre-treatment levels or normal levels for that patient population. By way of non-limiting example, the level of the marker of bone formation by 3 weeks after treatment is increased by, e.g., at least about 20% compared to pre-treatment levels or normal levels for that patient population. In one exemplary embodiment, the marker of bone resorption is serum level of C-telopeptide of type I collagen (CTX). In other exemplary embodiments, the marker of bone formation is bone-specific alkaline phosphatase (BSAP), osteocalcin (OstCa), and/or N-terminal extension of procollagen type 1 (P1NP).

The invention also provides a method of treating a bone-related disorder, wherein the method comprises administering to a human one or more amounts of a sclerostin inhibitor effective to increase bone mineral density for the total body (e.g., head, trunk, arms, and legs) or at the hip (e.g., total hip and/or femoral neck), spine (e.g., lumbar spine), wrist, finger, shin bone and/or heel by about 1%, about 2%, about 3%, about 4%, about 5%, about 6%, about 8%, about 10%, about 12%, about 15%, about 18%, about 20%, about 25%, or 30% or more. In some embodiments, the bone mineral density of the human before treatment is characteristic of osteoporosis or osteopenia, and one or more doses of sclerostin inhibitor are administered in an amount and for a time effective to

improve bone mineral density such that the bone mineral density is no longer characteristic of osteoporosis and/or osteopenia. For example, one or more doses may be administered for an initial time period to increase bone mineral density to within 2.5, or one, standard deviations of the density normal for a young adult (i.e., a T-score ≥ -2.5 or a T-score ≥ -1 , as defined below). In exemplary embodiments, the initial time period is about 3 months or less, 6 months or less, 9 months or less, 1 year or less, 18 months or less, or longer. The method may further comprise subsequently administering one or more amounts of a sclerostin inhibitor effective to maintain bone mineral density, optionally for a maintenance time period of at least about 6 months, 1 year, 2 years or longer (e.g., over the life-time of the subject).

The invention further provides a method of treating a bone-related disorder in a human by administering one or more doses between about 0.1 to about 20 mg/kg, or about 0.1 to about 12 mg/kg, or about 0.5 to about 12 mg/kg, or about 1 to about 10 mg/kg, or about 1 to about 8 mg/kg, or about 2 to about 8 mg/kg, or about 3 to about 8 mg/kg. In some embodiments, doses may be administered at an interval of about once 2 weeks or longer, once every month or longer, or once every 2 months or longer, or once every 3 months or longer, or once every 4 months or longer, or once every 5 months or longer, or once every 6 months or longer, or once every 9 months or longer, or once every year or longer. The sclerostin inhibitor may be used in the preparation of a medicament for administration using any of the dosing and timing regimens described herein. Optionally, the sclerostin inhibitor is presented in a container, such as a single dose or multidose vial, containing a dose of sclerostin inhibitor for administration (e.g., about 70 to about 450 mg of sclerostin inhibitor). In one exemplary embodiment, a vial may contain about 70 mg or 75 mg of sclerostin inhibitor, e.g. anti-sclerostin antibody, and would be suitable for administering a single dose of about 1 mg/kg. In other embodiments, a vial may contain about 140 mg or 150 mg; or about 210 mg or 220 mg or 250 mg; or about 280 mg or 290 mg or 300 mg; or about 350 mg or 360 mg; or about 420 mg or 430 mg or 440 mg or 450 mg of sclerostin inhibitor, e.g., anti-sclerostin antibody.

Additionally, the invention provides a method of treating a bone-related disorder in a human suffering from or at risk of hypocalcemia or hypercalcemia, a human in which treatment with a parathyroid hormone or analog thereof is contraindicated, or a human in which treatment with a bisphosphonate is contraindicated. The method comprises administering to the human an amount of a sclerostin inhibitor effective to increase the level of a marker of bone formation and/or reduce the level of a marker of bone resorption, without resulting in hypocalcemia or hypercalcemia (e.g., clinically-significant hypocalcemia or hypercalcemia).

The invention also provides a method of monitoring anti-sclerostin therapy, i.e., the physiological response to a sclerostin inhibitor. The method comprises the steps of administering one or more doses of a sclerostin inhibitor, and detecting the level of one or more markers of bone resorption, wherein a reduction of at least about 5%, about 10%, about 15%, about 20%, about 30%, about 40%, about 50% or more in the level of a marker of bone resorption, compared to pre-treatment levels or normal levels for that patient population, is indicative of effective treatment. The method optionally further comprises the step of detecting the level of one or more markers of bone formation, wherein an increase of at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, or about 100% in the level of a marker of bone formation, compared to pre-treatment levels or normal levels for that patient popula-

tion, is indicative of effective treatment. In certain embodiments, the increase in bone formation marker levels is about 20%. The method may further comprise the step of adjusting the dose of a sclerostin inhibitor to a different amount, e.g., higher if the change in bone resorption and/or bone formation is less than desired, or lower if the change in bone resorption and/or bone formation is more than desired.

In a different aspect, the invention provides selected sclerostin inhibitors that reduce the level of a marker of bone resorption by at least about 5%, about 10%, about 15%, about 20%, about 30%, about 40%, about 50% or more and increase the level of a marker of bone formation by at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, about 100%, or more, for at least about 1 week, about 2 weeks, about 1 month, about 6 weeks, about 2 months, about 10 weeks, or about 3 months. In a related aspect, the invention provides a method of selecting such sclerostin inhibitors by administering a candidate sclerostin inhibitor to an animal and selecting a candidate sclerostin inhibitor that changes the level of a marker of bone resorption and/or formation to the desired extent.

In any of the preceding methods or embodiments of the invention, the sclerostin inhibitor may be a sclerostin binding agent. The use of sclerostin binding agents disclosed in U.S. Patent Publication No. 20070110747, e.g., in any of the methods disclosed herein or for preparation of medicaments for administration according to any of the methods disclosed herein, is specifically contemplated. In this regard, the invention includes use of a sclerostin binding agent in preparation of a medicament for inhibiting bone resorption in an amount from about 1 mg/kg to about 10 mg/kg, wherein the amount is effective to reduce serum level of C-telopeptide of type 1 collagen (CTX) by at least 20%, compared to pre-treatment or normal levels, by 3 weeks after treatment begins. The invention also includes use of a sclerostin binding agent in preparation of a medicament for increasing bone mineral density in an amount from about 1 mg/kg to about 10 mg/kg, wherein the amount is effective to (a) reduce serum level of CTX by at least 20% compared to pre-treatment or normal levels, by 3 weeks after treatment begins, and (b) increase serum level of a bone formation marker selected from the group consisting of serum level of bone-specific alkaline phosphatase (BSAP), serum level of amino-terminal extension of peptide of pro-collagen type 1 (PINP), and serum level of osteocalcin (Ost*t*Ca), by at least 20%, compared to pre-treatment or normal levels, by 3 weeks after treatment begins.

The invention further includes use of a sclerostin binding agent in preparation of a medicament for treating a bone-related disorder in an amount from about 1 mg/kg to about 10 mg/kg for a first period of time, wherein the amount is effective to increase bone mineral density at the hip, spine, wrist, finger, shin bone and/or heel by at least about 3%, followed by an amount of from about 1 mg/kg to about 10 mg/kg for a second period of time effective to maintain bone mineral density. Use of a sclerostin binding agent in preparation of a medicament for treating a bone-related disorder in a human suffering from or at risk of hypocalcemia or hypercalcemia in an amount from about 1 mg/kg to about 10 mg/kg, also is contemplated, as well as use of a sclerostin binding agent in preparation of a medicament for treating a bone-related disorder in (a) a human in which treatment with a parathyroid hormone or analog thereof is contraindicated or (b) a human in which treatment with bisphosphonate is contraindicated.

The invention also includes containers comprising anti-sclerostin antibody or fragment thereof. In one embodiment, the container comprises anti-sclerostin antibody or fragment thereof and instructions for administering the antibody or

fragment thereof in an amount effective to (a) reduce serum level of C-telopeptide of type I collagen (CTX) by at least 20%, compared to pre-treatment or normal levels, by 3 weeks after treatment begins, and (b) increase serum level bone-specific alkaline phosphatase (BSAP), serum level of amino-terminal extension of peptide of procollagen type I (PINP), or serum level of osteocalcin (OstCa) by at least 20%, compared to pre-treatment or normal levels, by 3 weeks after treatment begins. Alternatively or in addition, the container comprises an amount of anti-sclerostin antibody from about 70 mg to about 450 mg. The invention further provides a container comprising anti-sclerostin antibody or fragment thereof and instructions for administering the antibody or fragment thereof for treating a bone-related disorder in an amount from about 1 mg/kg to about 10 mg/kg every two or four weeks. In addition, the invention provides a container comprising anti-sclerostin antibody or fragment thereof and instructions for administering the antibody or fragment thereof for treating a bone-related disorder in an amount from about 1 mg/kg to about 10 mg/kg for a period of about 3 months.

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1 is a graph of percent change of N-terminal extension of procollagen type 1 (PINP) levels compared to baseline and placebo PINP levels versus time (day) post-administration of various single doses of a sclerostin binding agent in healthy, postmenopausal women.

FIG. 2 is a graph of percent change of bone-specific alkaline phosphatase (BSAP) levels compared to baseline and placebo BSAP levels versus time (day) post-administration of various single doses of a sclerostin binding agent in healthy, postmenopausal women.

FIG. 3 is a graph of percent change of osteocalcin levels compared to baseline and placebo osteocalcin levels versus time (day) post-administration of various single doses of a sclerostin binding agent in healthy, postmenopausal women.

FIG. 4 is a graph of percent change of serum C-terminal telopeptide of type 1 collagen (CTX) levels compared to baseline and placebo serum CTX levels versus time (day) post-administration of various single doses of a sclerostin binding agent in healthy, postmenopausal women.

FIG. 5 are graphs of percent change of osteocalcin, BSAP, PINP, and CTX levels compared to baseline and placebo levels versus time (day) post-administration of a single dose of 5 mg/kg or 10 mg/kg of sclerostin binding agent in healthy, postmenopausal women.

FIG. 6 is a graph of percent change of serum calcium levels compared to baseline and placebo serum calcium levels versus time (day) post-administration of various single doses of a sclerostin binding agent in healthy, postmenopausal women.

FIG. 7 are graphs of percent change of bone mineral density compared to baseline and placebo versus time (day) post-administration of various single doses of sclerostin binding agent in healthy, postmenopausal women.

DETAILED DESCRIPTION OF THE INVENTION

The invention is predicated, at least in part, on the surprising discovery that blocking or inhibiting the biological activity of human sclerostin triggers multiple physiological responses linked to increased bone mineral density (BMD), including significant inhibition of bone resorption. Most currently available therapies only inhibit bone resorption without increasing bone formation. Some currently available therapies for disorders associated with reduced BMD only

increase bone formation without significantly reducing bone resorption. For example, when bone formation is triggered by some current drugs, bone resorption may also increase (albeit potentially at a lower rate than before therapy). In contrast, agents that interfere with sclerostin activity both enhance bone formation and reduce bone resorption. In other words, sclerostin inhibitors “uncouple” bone formation and bone resorption to more effectively build bone. The materials and methods of the invention are superior to existing therapies whose therapeutic efficacy is limited and which are accompanied by potentially serious adverse side effects.

In this regard, the invention provides a method of inhibiting bone resorption, e.g., bone resorption mediated by osteoclasts, bone cells that dissolve bone mineral matrices. The invention further provides a method of ameliorating the effects of an osteoclast-related disorder, i.e., a disorder caused by abnormally increased osteoclast activity that, in some embodiments, manifests as abnormally high bone resorption. The inventive method comprises administering to 15 a human an amount of sclerostin binding agent that reduces the level of a marker of bone resorption and, optionally, increases the level of a marker of bone formation.

Activity of a sclerostin inhibitor, e.g., a sclerostin binding agent, (further described below) may be measured in a variety 20 of ways. Sclerostin binding agent-mediated increases in bone mineral content or bone density may be measured using single- and dual-energy X-ray absorptometry, ultrasound, computed tomography, radiography, and magnetic resonance imaging. The amount of bone mass may also be calculated 25 from body weights or by using other methods (see Guinness-Hey, *Metab. Bone Dis. Relat. Res.*, 5:177-181 (1984)). Animals and particular animal models are used in the art for testing the effect of the pharmaceutical compositions and methods on, for example, parameters of bone loss, bone 30 resorption, bone formation, bone strength, or bone mineralization that mimic conditions of human disease such as osteoporosis and osteopenia. Examples of such models include the ovariectomized rat model (Kalu, *Bone and Mineral*, 15:175-192 (1991); Frost and Jee, *Bone and Mineral*, 40 18:227-236 (1992); and Jee and Yao, *J. Musculoskel. Neuron. Interact.*, 1:193-207 (2001)). The methods for measuring sclerostin binding agent activity described herein also may be used to determine the efficacy of other sclerostin inhibitors.

In humans, bone mineral density can be determined clinically 45 using dual x-ray absorptiometry (DXA) of, for example, the hip and spine. Other techniques include quantitative computed tomography (QCT), ultrasonography, single-energy x-ray absorptiometry (SXA), and radiographic absorptiometry. Common central skeletal sites for measurement include 50 the spine and hip; peripheral sites include the forearm, finger, wrist and heel. Except for ultrasonography, the American Medical Association notes that BMD techniques typically involve the use of x-rays and are based on the principle that attenuation of the radiation depends on thickness and composition of the tissues in the radiation path. All techniques 55 involve the comparison of results to a normative database.

Alternatively, a physiological response to one or more sclerostin binding agents can be gauged by monitoring bone 60 marker levels. Bone markers are products created during the bone remodeling process and are released by bone, osteoblasts, and/or osteoclasts. Fluctuations in bone resorption and/or bone formation “marker” levels imply changes in bone 65 remodeling/modeling. The International Osteoporosis Foundation (IOF) recommends using bone markers to monitor bone density therapies (see, e.g., Delmas et al., *Osteoporos Int.*, Suppl. 6:S2-17 (2000), incorporated herein by reference). Markers indicative of bone resorption (or osteoclast

activity) include, for example, C-telopeptide (e.g., C-terminal telopeptide of type I collagen (CTX) or serum cross-linked C-telopeptide), N-telopeptide (N-terminal telopeptide of type I collagen (NTX)), deoxypyridinoline (DPD), pyridinoline, urinary hydroxyproline, galactosyl hydroxylysine, and tartrate-resistant acid phosphatase (e.g., serum tartrate-resistant acid phosphatase isoform 5b). Bone formation/mineralization markers include, but are not limited to, bone-specific alkaline phosphatase (BSAP), peptides released from N- and C-terminal extension of type I procollagen (P1NP, PICP), and osteocalcin (OstCa). Several kits are commercially-available to detect and quantify markers in clinical samples, such as urine and blood.

Upon administration, the sclerostin binding agent preferably reduces the level of one or more markers of bone resorption, such as the serum level of C-telopeptide of type I collagen (CTX). Accordingly, the invention further provides a method of monitoring anti-sclerostin therapy, i.e., the physiological response to a sclerostin binding agent or other sclerostin inhibitor. The method comprises administering a sclerostin binding agent, then measuring the level of one or more markers of bone resorption. In addition, the method can comprise measuring the level of one or more markers of bone formation before administration of a sclerostin binding agent. The level of bone resorption marker during and/or after treatment with the sclerostin binding agent may be compared to a pre-treatment level, or alternatively may be compared to a standard range typical of that patient population. One of ordinary skill in the art can readily determine a suitable standard range by testing a representative number of patients of like age, gender, disease level, and/or other characteristics of the patient population. The level of bone resorption marker can be reduced by at least about 5% (e.g., about 10%, about 20%, or about 30%) by a single dose of sclerostin binding agent. In some embodiments, the dose of sclerostin binding agent reduces the level of bone resorption marker at least about 40% (e.g., about 50%, about 60%, or about 70%) compared to the level of the bone resorption marker prior to administering the sclerostin binding agent. In addition, the bone resorption marker level may be reduced for at least about 3 days (e.g., about 7 days, about 2 weeks, about 3 weeks, about 1 month, about 5 weeks, about 6 weeks, about 7 weeks, about 2 months, about 9 weeks, about 10 weeks, about 11 weeks, or about 3 months) after administration of a single dose of the sclerostin binding agent.

In addition to decreasing the level of bone resorption markers, the amount of sclerostin binding agent administered to a patient also can increase the level of one or more markers of bone formation, such as the serum level of BSAP, the serum level of P1NP, and/or the serum level of OstCa. A single dose of sclerostin binding agent can increase the level of a bone formation marker by, for example, at least about 5% (e.g., about 10%, about 20%, or about 30%). In some embodiments, the dose of sclerostin binding agent elevates the level of a bone formation marker at least about 40% (e.g., about 50%, about 60%, or about 70%). In other embodiments, the dose of sclerostin binding agent increases the level of one or more bone formation markers by at least about 75% (e.g., about 80%, about 90%, about 100%, or about 110%). In yet other embodiments, the dose of sclerostin binding agent increases the level of a bone formation marker by at least about 120% (e.g., about 130%, about 140%, about 150%, about 160% or about 170%). In alternative embodiments, the sclerostin binding agent increases the level of bone formation marker by least about 180% (e.g., about 190% or about 200%). Bone formation marker levels ideally remain elevated (compared to bone formation marker levels pre-treatment or

to a standard range typical of that patient population) for at least about 3 days (e.g., about 7 days, about 2 weeks, about 3 weeks, about 1 month, about 5 weeks, about 6 weeks, about 7 weeks, about 2 months, about 9 weeks, about 10 weeks, about 11 weeks, or about 3 months) after administration of a single dose of the sclerostin binding agent.

The invention also provides a method of increasing bone mineral density (BMD), wherein an amount of sclerostin binding agent that (a) reduces the level of a marker of bone resorption and (b) increases the level of a marker of bone formation is administered to a human. BMD generally correlates with skeletal fragility and osteoporosis. Typically, BMD is measured “total body” (e.g., head, trunk, arms, and legs) or at the hip (e.g., total hip and/or femoral neck), spine (e.g., lumbar spine), wrist, finger, shin bone and/or heel. In osteoporosis diagnosis, a patient’s BMD is compared to the peak density of a 30-year old healthy adult (i.e., a “young adult”), creating the so-called “T-score.” A patient’s BMD also may be compared to an “age-matched” bone density (see, e.g., World Health Organization Scientific Group on the Prevention and Management of Osteoporosis, “Prevention and management of osteoporosis: report of a WHO scientific group,” *WHO Technical Report Series*; 921, Geneva, Switzerland (2000)). The difference between a patient’s BMD and that of a healthy, young adult is conventionally referred to in terms of the multiple of a “standard deviation,” which typically equals about 10% to about 12% decrease in bone density. The World Health Organization proposed four diagnostic categories based on BMD T-scores. A BMD value within 1 standard deviation of the young adult reference mean (T-score ≥ -1) is “normal.” Low bone mass (osteopenia) is indicated by a BMD value more than 1 standard deviation below the young adult mean, but less than 2 standard deviations (T-score < -1 and > -2.5). A T-score of more than 2.5 standard deviations below the norm supports a diagnosis of osteoporosis. If a patient additionally suffers from one or more fragility fractures, the patient qualifies as having severe osteoporosis.

The sclerostin inhibitor, e.g., a sclerostin binding agent, may be administered to a patient to improve bone mineral density regardless of the patient’s T-score. The sclerostin binding agent may be administered at a dose and for a time period effective to increase BMD in the patient by at least about 1% (about 2%, about 3%, about 4%, about 5%, or about 6%). In some embodiments, BMD is increased by at least about 8% (e.g., at least about 10%, about 12%, about 15%, or about 18%). In other embodiments, BMD is increased by the sclerostin binding agent at least about 20% (e.g., at least about 22%, about 25%, or about 28%) at the hip, spine, wrist, finger, shin bone, and/or heel. In yet other embodiments, BMD is increased at least about 30% (e.g., at least about 32%, about 35%, about 38%, or about 40%). In other words, the BMD can be increased to the range of about 1 to about 2.5 standard deviations (preferably a range of about 0 to about 1 standard deviations) below the normal BMD of a healthy young adult.

Alterations in bone remodeling can lead to fluctuations in mineral concentrations throughout the body. Bone is one of the principal regulators of calcium levels in the bloodstream. Osteoclast-mediated bone resorption releases stored calcium into the systemic circulation, while osteoblast-mediated bone formation removes calcium from circulation to incorporate into bone tissue. In normal bone remodeling, these processes cycle to maintain healthy, strong bone and maintain free calcium levels at about 8.5 mg/dL to about 10.5 mg/dL (e.g., about 2.2 mmol/L to about 2.6 mmol/L). Bone disorders, other illnesses, and even certain therapies can disrupt systemic calcium levels with dire consequences. Hypercalcemia

is associated with high levels of calcium in the blood (e.g., greater than 12 mg/dL or 3 mmol/L). Extraordinarily high calcium levels leads to, for example, fatigue, confusion, constipation, decreased appetite, frequent urination, heart problems, and bone pain. Hypocalcemia is an electrolyte imbalance indicated by an abnormally low level of calcium in the blood (e.g., less than about 9 mg/dL or 2.2 mmol/L). Calcium levels of <7.5 mg/dL (<1.87 mmol/L) or less are considered severe hypocalcemia and may be accompanied by clinical symptoms.

Common symptoms of hypocalcemia include nerve and muscle spasms and cramps, numbness, tingling in the extremities, confusion, and heart irregularities. Extreme variations in system calcium can lead to coma and death.

Several ailments and pharmaceutical therapies alter system calcium levels. Hypercalcemia and hypocalcemia can result from, for example, chronic kidney disease, renal failure, primary or secondary hyperparathyroidism, pseudohyperparathyroidism, hypoparathyroidism, pseudohypoparathyroidism, magnesium depletion, alcoholism, bisphosphonate therapy, severe hypermagnesemia, vitamin D deficiency, hyperphosphatemia, acute pancreatitis, hungry bone syndrome, chelation, osteoblastic metastases, sepsis, surgery, chemotherapy, neoplasia syndrome, familial hypocalciuric hypercalcemia, sarcoidosis, tuberculosis, berylliosis, histoplasmosis, Candidiasis, Coccidioidomycosis, histiocytosis X, Hodgkin's or Non-Hodgkin's lymphoma, Crohn's disease, Wegener's granulomatosis, leukemia, pneumonia, silicone-induced granulomas, immobilization, or drug therapy, such as administration of thiazide diuretics, lithium, estrogens, fluorides, glucose, and insulin. In addition, serum calcium fluctuations are a side effect of many existing bone-related therapies, such as bisphosphonate and parathyroid hormone therapy. Because of the potentially life-threatening consequences of calcium imbalance, patients susceptible to hypocalcemia or hypercalcemia may need to forego certain therapy options.

Remarkably, sclerostin inhibitors, e.g., sclerostin binding agents, have been shown to promote bone formation and inhibit (or slow) bone resorption with minimal fluctuations in systemic calcium levels (e.g., calcium levels fluctuate 10% or less from baseline serum calcium levels). Accordingly, the materials and method of the invention are particularly advantageous in treating patients that are susceptible or sensitive to unstable calcium levels. The amount of sclerostin binding agent administered to a human in the context of this aspect of the invention is an amount that does not result in hypocalcemia or hypercalcemia (e.g., clinically-significant hypocalcemia or hypercalcemia). In addition, the invention provides a method of treating a bone-related disorder in a human suffering from or at risk of hypocalcemia or hypercalcemia or a human in which treatment with bisphosphonate, a parathyroid hormone, or parathyroid hormone analog is contraindicated. The method comprises administering to the human an amount of a sclerostin binding agent effective to increase the level of a marker of bone formation, such as serum levels of B SAP, P1NP, and/or OstCa and/or reduce the level of a marker of bone resorption, such as CTX.

The inventive method is useful for treating or preventing bone-related disorders, such as bone-related disorders associated with abnormal osteoblast or osteoclast activity. Indeed, the sclerostin inhibitor (e.g., sclerostin binding agent) can be administered to a human suffering from a bone related disorder selected from the group consisting of achondroplasia, cleidocranial dysostosis, enchondromatosis, fibrous dysplasia, Gaucher's Disease, hypophosphatemic rickets, Marfan's syndrome, multiple hereditary exostoses, neurofibromatosis,

osteogenesis imperfecta, osteopetrosis, osteopoikilosis, sclerotic lesions, pseudoarthrosis, pyogenic osteomyelitis, periodontal disease, anti-epileptic drug induced bone loss, primary and secondary hyperparathyroidism, familial hyperparathyroidism syndromes, weightlessness induced bone loss, osteoporosis in men, postmenopausal bone loss, osteoarthritis, renal osteodystrophy, infiltrative disorders of bone, oral bone loss, osteonecrosis of the jaw, juvenile Paget's disease, melorheostosis, metabolic bone diseases, mastocytosis, sickle cell anemia/disease, organ transplant related bone loss, kidney transplant related bone loss, systemic lupus erythematosus, ankylosing spondylitis, epilepsy, juvenile arthritides, thalassemia, mucopolysaccharidoses, Fabry Disease, Turner Syndrome, Down Syndrome, Klinefelter Syndrome, leprosy, Perthe's Disease, adolescent idiopathic scoliosis, infantile onset multi-system inflammatory disease, Winchester Syndrome, Menkes Disease, Wilson's Disease, ischemic bone disease (such as Legg-Calve-Perthes disease and regional migratory osteoporosis), anemic states, conditions caused by steroids, glucocorticoid-induced bone loss, heparin-induced bone loss, bone marrow disorders, scurvy, malnutrition, calcium deficiency, osteoporosis, osteopenia, alcoholism, chronic liver disease, postmenopausal state, chronic inflammatory conditions, rheumatoid arthritis, inflammatory bowel disease, ulcerative colitis, inflammatory colitis, Crohn's disease, oligomenorrhea, amenorrhea, pregnancy, diabetes mellitus, hyperthyroidism, thyroid disorders, parathyroid disorders, Cushing's disease, acromegaly, hypogonadism, immobilization or disuse, reflex sympathetic dystrophy syndrome, regional osteoporosis, osteomalacia, bone loss associated with joint replacement, HIV associated bone loss, bone loss associated with loss of growth hormone, bone loss associated with cystic fibrosis, chemotherapy-associated bone loss, tumor-induced bone loss, cancer-related bone loss, hormone ablative bone loss, multiple myeloma, drug-induced bone loss, anorexia nervosa, disease-associated facial bone loss, disease-associated cranial bone loss, disease-associated bone loss of the jaw, disease-associated bone loss of the skull, bone loss associated with aging, facial bone loss associated with aging, cranial bone loss associated with aging, jaw bone loss associated with aging, skull bone loss associated with aging, and bone loss associated with space travel.

The inventive method need not cure the patient of the disorder or completely protect against the onset of a bone-related disorder to achieve a beneficial biological response. The method may be used prophylactically, meaning to protect, in whole or in part, against a bone-related disorder or symptom thereof. The method also may be used therapeutically to ameliorate, in whole or in part, a bone-related disorder or symptom thereof, or to protect, in whole or in part, against further progression of a bone-related disorder or symptom thereof. Indeed, the materials and methods of the invention are particularly useful for increasing bone mineral density and maintaining the increased BMD over a period of time. In this regard, the invention provides a method of treating a bone-related disorder, which method comprises (a) administering one or more amounts of a sclerostin binding agent effective to increase BMD measured for the total body (e.g., head, trunk, arms, and legs) or at the hip (e.g., total hip and/or femoral neck), spine (e.g., lumbar spine), wrist, finger, shin bone and/or heel by about 1%, about 2%, about 3%, about 6%, about 8%, about 10%, about 12%, about 15%, about 18%, about 20%, about 25%, or 30% or more. One or more administrations of a pharmaceutical composition comprising the sclerostin binding agent may be carried out over a therapeutic period of, for example, about 1 month to about 12

11

months (e.g., about 2 months, about 3 months, about 4 months, about 5 months, about 6 months, about 7 months, about 8 months, about 9 months, about 10 months, or about 11 months). The method further includes (b) subsequently administering one or more amounts of a sclerostin binding agent effective to maintain bone mineral density. By "maintain bone mineral density" is meant that the increased BMD resulting from step (a) does not fall more than about 1% to about 5% over the course of step (b) (e.g., about 6 months, about 9 months about 1 year, about 18 months, about 2 years, or over the course of the patient's life). It will be appreciated that a patient can require alternate treatment phases for increasing bone density and maintaining bone density.

The sclerostin binding agent is preferably administered to a patient in a physiologically-acceptable (e.g., pharmaceutical) composition, which can include carriers, excipients, or diluents. It will be appreciated that the sclerostin binding agents described herein may be used in the preparation of a medicament for administration using any of the dosage and timing regimens disclosed herein. Pharmaceutical compositions and methods of treatment are disclosed in U.S. Patent Publication No. 20050106683, which is incorporated by reference herein. "Physiologically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human. In addition, the composition administered to a subject may contain more than one sclerostin inhibitor (e.g., a sclerostin binding agent and a synthetic chemical sclerostin inhibitor) or a sclerostin inhibitor in combination with one or more therapeutics having different mechanisms of action.

The development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including e.g., subcutaneous, oral, parenteral, intravenous, intranasal, and intramuscular administration and formulation, is well known in the art and discussed in U.S. Patent Publication No. 20070110747. For example, in certain circumstances, it will be desirable to deliver a pharmaceutical composition comprising a sclerostin binding agent subcutaneously, parenterally, intravenously, intramuscularly, or even intraperitoneally. Such approaches are well known to the skilled artisan, some of which are further described, for example, in U.S. Pat. Nos. 5,543,158; 5,641,515; and 5,399,363. Illustrative pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (for example, see U.S. Pat. No. 5,466,468). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists.

In one embodiment, for parenteral administration in an aqueous solution, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous, and intraperitoneal administration. For example, one dose may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion (see, for example, Remington's Pharmaceutical Sciences, 15th ed., Mack Pub. Co., Easton, Pa., pp. 1035-1038 and 1570-1580). Some variation in dosage and frequency of administration may occur depending on the condition of the subject being treated; age, height, weight, and overall health of the patient; and the existence of any side effects. In addition, a pharmaceutical composition comprising a sclerostin binding agent may be placed within containers (e.g., vials), along with packaging material that provides instructions regarding the

12

use of such pharmaceutical compositions. Generally, such instructions will include a tangible expression describing the reagent concentration, as well as within certain embodiments, relative amounts of excipient ingredients or diluents (e.g., water, saline or PBS) that may be necessary to reconstitute the pharmaceutical composition.

The sclerostin binding agent is administered in an amount that reduces the level of a bone resorption marker and/or increases the level of a bone formation marker and/or increases bone density. The dose of sclerostin binding agent administered may range from about 0.5 mg/kg to about 20 mg/kg (e.g., 12 mg/kg) of body weight. For example, the dose of sclerostin binding agent may range from about 1 mg/kg to about 10 mg/kg (e.g., about 2 mg/kg or about 9 mg/kg), about 1 mg/kg to about 3 mg/kg, or about 3 mg/kg to about 8 mg/kg (e.g., about 4 mg/kg, 5 mg/kg, 6 mg/kg, or 7 mg/kg).

In addition, it may be advantageous to administer multiple doses of a sclerostin binding agent or space out the administration of doses, depending on the therapeutic regimen selected for a particular patient. The sclerostin binding agent can be administered periodically over a time period of one year or less (e.g., 9 months or less, 6 months or less, or 3 months or less). In this regard, the sclerostin binding agent can be administered to the human once every about 7 days, or 2 weeks, or 3 weeks, or 1 month, or 5 weeks, or 6 weeks, or 7 weeks, or 2 months, or 9 weeks, or 10 weeks, or 11 weeks, or 3 months, or 13 weeks, or 14 weeks, or 15 weeks, or 4 months, or 17 weeks, or 18 weeks, or 19 weeks, or 5 months, or 21 weeks, or 22 weeks, or 23 weeks, or 6 months, or 12 months.

The inventive method comprises administering an amount of a "sclerostin inhibitor." As used herein, the term "sclerostin inhibitor" means any molecule that inhibits the biological activity of sclerostin on bone, as measured by changes to bone mineralization, bone density, effect on osteoblasts and/or osteoclasts, markers of bone formation, markers of bone resorption, markers of osteoblast activity, and/or markers of osteoclast activity. Such inhibitors may act by binding to sclerostin or its receptor or binding partner. Inhibitors in this category include "sclerostin binding agents," such as, e.g., antibodies or peptide-based molecules. "Sclerostin inhibitors" also refers to small organic chemical compounds, optionally of less than about 1000 Daltons in molecular weight that bind sclerostin and inhibit its activity. Inhibitors may alternatively act by inhibiting expression of sclerostin. Inhibitors in this category include polynucleotides or oligonucleotides that bind to sclerostin DNA or mRNA and inhibit sclerostin expression, including an antisense oligonucleotide, inhibitory RNA, DNA enzyme, ribozyme, an aptamer or pharmaceutically acceptable salts thereof that inhibit the expression of sclerostin.

A "sclerostin binding agent" specifically binds to sclerostin or portions thereof to block or impair binding of human sclerostin to one or more ligands. Sclerostin, the product of the SOST gene, is absent in sclerosteosis, a skeletal disease characterized by bone overgrowth and strong dense bones (Brunkow et al., *Am. J. Hum. Genet.*, 68:577-589 (2001); Balemans et al., *Hum. Mol. Genet.*, 10:537-543 (2001)). The amino acid sequence of human sclerostin is reported by Brunkow et al. and is disclosed in U.S. Patent Publication No. 20070110747 as SEQ ID NO: 1 (which patent publication is incorporated in its entirety for its description of sclerostin binding agents and Sequence Listing). Recombinant human sclerostin/SOST is commercially available from R&D Systems (Minneapolis, Minn., USA; 2006 Catalog #1406-ST-025). Additionally, recombinant mouse sclerostin/SOST is commercially available from R&D Systems (Minneapolis, Minn., USA; 2006 Catalog #1589-ST-025). Research grade

sclerostin-binding monoclonal antibodies are commercially available from R&D Systems (Minneapolis, Minn., USA; mouse monoclonal: 2006 Catalog #MAB1406; rat monoclonal: 2006 Catalog #MAB1589). U.S. Pat. Nos. 6,395,511 and 6,803,453, and U.S. Patent Publication Nos. 20040009535 and 20050106683 refer to anti-sclerostin antibodies generally. Examples of sclerostin binding agents suitable for use in the context of the invention also are described in U.S. Patent Publication Nos. 20070110747 and 20070072797, which are hereby incorporated by reference. Additional information regarding materials and methods for generating sclerostin binding agents can be found in U.S. Patent Publication No. 20040158045.

The sclerostin binding agent of the invention preferably is an antibody. The term “antibody” refers to an intact antibody, or a binding fragment thereof. An antibody may comprise a complete antibody molecule (including polyclonal, monoclonal, chimeric, humanized, or human versions having full length heavy and/or light chains), or comprise an antigen binding fragment thereof. Antibody fragments include F(ab')₂, Fab, Fab', Fv, Fc, and Fd fragments, and can be incorporated into single domain antibodies, single-chain antibodies, maxibodies, minibodies, intrabodies, diabodies, triabodies, tetrabodies, v-NAR and bis-scFv (see, e.g., Hollinger and Hudson, *Nature Biotechnology*, 23(9):1126-1136 (2005)). Antibody polypeptides, including fibronectin polypeptide monobodies, also are disclosed in U.S. Pat. No. 6,703,199. Other antibody polypeptides are disclosed in U.S. Patent Publication No. 20050238646. Anti-sclerostin antibodies may bind to sclerostin of SEQ ID NO: 1, or a naturally occurring variant thereof, with an affinity of less than or equal to 1×10^{-7} M, less than or equal to 1×10^{-8} M, less than or equal to 1×10^{-9} M, less than or equal to 1×10^{-10} M, less than or equal to 1×10^{-11} M, or less than or equal to 1×10^{-12} M. Affinity may be determined by an affinity ELISA assay. In certain embodiments, affinity may be determined by a BIACore assay. In certain embodiments, affinity may be determined by a kinetic method. In certain embodiments, affinity may be determined by an equilibrium/solution method.

An antibody fragment may be any synthetic or genetically engineered protein. For example, antibody fragments include isolated fragments consisting of the light chain variable region, “Fv” fragments consisting of the variable regions of the heavy and light chains, recombinant single chain polypeptide molecules in which light and heavy variable regions are connected by a peptide linker (scFv proteins).

Another form of an antibody fragment is a peptide comprising one or more complementarity determining regions (CDRs) of an antibody. CDRs (also termed “minimal recognition units” or “hypervariable region”) can be obtained by constructing polynucleotides that encode the CDR of interest. Such polynucleotides are prepared, for example, by using the polymerase chain reaction to synthesize the variable region using mRNA of antibody-producing cells as a template (see, for example, Larrick et al., *Methods: A Companion to Methods in Enzymology*, 2:106 (1991); Courtenay-Luck, “Genetic Manipulation of Monoclonal Antibodies,” in *Monoclonal Antibodies Production, Engineering and Clinical Application*, Ritter et al. (eds.), page 166, Cambridge University Press (1995); and Ward et al., “Genetic Manipulation and Expression of Antibodies,” in *Monoclonal Antibodies: Principles and Applications*, Birch et al., (eds.), page 137, Wiley-Liss, Inc. (1995)).

In one embodiment of the invention, the sclerostin binding agent cross-blocks the binding of at least one of antibodies Ab-A, Ab-B, Ab-C, Ab-D, Ab-1, Ab-2, Ab-3, Ab-4, Ab-5, Ab-6, Ab-7, Ab-8, Ab-9, Ab-10, Ab-11, Ab-12, Ab-13,

Ab-14, Ab-15, Ab-16, Ab-17, Ab-18, Ab-19, Ab-20, Ab-21, Ab-22, Ab-23, and Ab-24 (all of which are described in U.S. Patent Publication No. 20070110747) to sclerostin. Alternatively or in addition, the sclerostin binding agent is cross-blocked from binding to sclerostin by at least one of antibodies Ab-A, Ab-B, Ab-C, Ab-D, Ab-1, Ab-2, Ab-3, Ab-4, Ab-5, Ab-6, Ab-7, Ab-8, Ab-9, Ab-10, Ab-11, Ab-12, Ab-13, Ab-14, Ab-15, Ab-16, Ab-17, Ab-18, Ab-19, Ab-20, Ab-21, Ab-22, Ab-23, and Ab-24 (all of which are described in U.S. Patent Publication No. 20070110747). The terms “cross-block,” “cross-blocked,” and “cross-blocking” are used interchangeably herein to mean the ability of an antibody or other binding agent to interfere with the binding of other antibodies or binding agents to sclerostin. The extent to which an antibody or other binding agent is able to interfere with the binding of another to sclerostin, and therefore whether it can be said to cross-block, can be determined using competition binding assays. In some aspects of the invention, a cross-blocking antibody or fragment thereof reduces sclerostin binding of a reference antibody between about 40% and about 100%, such as about 60% and about 100%, specifically between 70% and 100%, and more specifically between 80% and 100%. A particularly suitable quantitative assay for detecting cross-blocking uses a BIACore machine which measures the extent of interactions using surface plasmon resonance technology. Another suitable quantitative cross-blocking assay uses an ELISA-based approach to measure competition between antibodies or other binding agents in terms of their binding to sclerostin.

Suitable sclerostin binding agents include antibodies and portions thereof described in U.S. Patent Publication No. 20070110747, such as one or more of CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2 and CDR-L3 as specifically disclosed therein. At least one of the regions of CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 may have at least one amino acid substitution, provided that the binding agent retains the binding specificity of the non-substituted CDR. The non-CDR portion of the binding agent may be a non-protein molecule, wherein the binding agent cross-blocks the binding of an antibody disclosed herein to sclerostin and/or neutralizes sclerostin. The non-CDR portion of the binding agent may be a non-protein molecule in which the binding agent exhibits a similar binding pattern to human sclerostin peptides in a human sclerostin peptide epitope competition binding assay as that exhibited by at least one of antibodies Ab-A, Ab-B, Ab-C, Ab-D, Ab-1, Ab-2, Ab-3, Ab-4, Ab-5, Ab-6, Ab-7, Ab-8, Ab-9, Ab-10, Ab-11, Ab-12, Ab-13, Ab-14, Ab-15, Ab-16, Ab-17, Ab-18, Ab-19, Ab-20, Ab-21, Ab-22, Ab-23, and Ab-24 (all of which are described in U.S. Patent Publication No. 20070110747), and/or neutralizes sclerostin. The non-CDR portion of the binding agent may be composed of amino acids, wherein the binding agent is a recombinant binding protein or a synthetic peptide, and the recombinant binding protein cross-blocks the binding of an antibody to sclerostin and/or neutralizes sclerostin. The non-CDR portion of the binding agent may be composed of amino acids, wherein the binding agent is a recombinant binding protein, and the recombinant binding protein exhibits a similar binding pattern to human sclerostin peptides in the human sclerostin peptide epitope competition binding assay (described in U.S. Patent Publication No. 20070110747) as that exhibited by at least one of the antibodies Ab-A, Ab-B, Ab-C, Ab-D, Ab-1, Ab-2, Ab-3, Ab-4, Ab-5, Ab-6, Ab-7, Ab-8, Ab-9, Ab-10, Ab-11, Ab-12, Ab-13, Ab-14, Ab-15, Ab-16, Ab-17, Ab-18, Ab-19, Ab-20, Ab-21, Ab-22, Ab-23, and Ab-24 (described in U.S. Patent Publication No. 20070110747), and/or neutralizes sclerostin. Preferably, the

15

sclerostin binding agent is Ab-A, Ab-B, Ab-C, Ab-D, Ab-1, Ab-2, Ab-3, Ab-4, Ab-5, Ab-6, Ab-7, Ab-8, Ab-9, Ab-10, Ab-11, Ab-12, Ab-13, Ab-14, Ab-15, Ab-16, Ab-17, Ab-18, Ab-19, Ab-20, Ab-21, Ab-22, Ab-23, or Ab-24 of U.S. Patent Publication No. 20070110747.

In addition, the sclerostin binding agent can comprise at least one CDR sequence having at least 75% identity (e.g., 100% identity) to a CDR selected from SEQ ID NOs: 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 78, 79, 80, 81, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 137, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 351, 352, 353, 358, 359, and 360 disclosed in U.S. Patent Publication No. 20070110747. Preferably, the sclerostin binding agent comprises at least one CDR sequence having at least 75% identity to a CDR selected from SEQ ID NOs: 245, 246, 247, 78, 79, 80, 269, 270, 271, 239, 240, and 24, all of which is described in U.S. Patent Publication No. 20070110747. As described in U.S. Patent Publication No. 20070110747, the sclerostin binding agent can comprise: a) CDR sequences of SEQ ID NOs: 54, 55, and 56 and CDR sequences of SEQ ID NOs: 51, 52, and 53; b) CDR sequences of SEQ ID NOs: 60, 61, and 62 and CDR sequences of SEQ ID NOs: 57, 58, and 59; c) CDR sequences of SEQ ID NOs: 48, 49, and 50 and CDR sequences of SEQ ID NOs: 45, 46, and 47; d) CDR sequences of SEQ ID NOs: 42, 43, and 44 and CDR sequences of SEQ ID NOs: 39, 40, and 41; e) CDR sequences of SEQ ID NOs: 275, 276, and 277 and CDR sequences of SEQ ID NOs: 287, 288, and 289; f) CDR sequences of SEQ ID NOs: 278, 279, and 280 and CDR sequences of SEQ ID NOs: 290, 291, and 292; g) CDR sequences of SEQ ID NOs: 78, 79, and 80 and CDR sequences of SEQ ID NOs: 245, 246, and 247; h) CDR sequences of SEQ ID NOs: 81, 99, and 100 and CDR sequences of SEQ ID NOs: 248, 249, and 250; i) CDR sequences of SEQ ID NOs: 101, 102, and 103 and CDR sequences of SEQ ID NOs: 251, 252, and 253; j) CDR sequences of SEQ ID NOs: 104, 105, and 106 and CDR sequences of SEQ ID NOs: 254, 255, and 256; k) CDR sequences of SEQ ID NOs: 107, 108, and 109 and CDR sequences of SEQ ID NOs: 257, 258, and 259; l) CDR sequences of SEQ ID NOs: 110, 111, and 112 and CDR sequences of SEQ ID NOs: 260, 261, and 262; m) CDR sequences of SEQ ID NOs: 281, 282, and 283 and CDR sequences of SEQ ID NOs: 293, 294, and 295; n) CDR sequences of SEQ ID NOs: 113, 114, and 115 and CDR sequences of SEQ ID NOs: 263, 264, and 265; o) CDR sequences of SEQ ID NOs: 284, 285, and 286 and CDR sequences of SEQ ID NOs: 296, 297, and 298; p) CDR sequences of SEQ ID NOs: 116, 237, and 238 and CDR sequences of SEQ ID NOs: 266, 267, and 268; q) CDR sequences of SEQ ID NOs: 239, 240, and 241 and CDR sequences of SEQ ID NOs: 269, 270, and 271; r) CDR sequences of SEQ ID NOs: 242, 243, and 244 and CDR sequences of SEQ ID NOs: 272, 273, and 274; or s) CDR sequences of SEQ ID NOs: 351, 352, and 353 and CDR sequences of SEQ ID NOs: 358, 359, and 360.

The sclerostin binding agent also can comprise at least one CDR sequence having at least 75% identity to a CDR selected from CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and CDR-L3 wherein CDR-H1 has the sequence given in SEQ ID NO: 245 or SEQ ID NO: 269, CDR-H2 has the sequence given in SEQ ID NO: 246 or SEQ ID NO: 270, CDR-H3 has the sequence given in SEQ ID NO: 247 or SEQ ID NO: 271,

16

CDR-L1 has the sequence given in SEQ ID NO: 78 or SEQ ID NO: 239, CDR-L2 has the sequence given in SEQ ID NO: 79 or SEQ ID NO: 240 and CDR-L3 has the sequence given in SEQ ID NO: 80 or SEQ ID NO: 241, all of which is described in U.S. Patent Publication No. 20070110747.

Alternatively, the sclerostin binding agent can have a heavy chain comprising CDR's H1, H2, and H3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 137 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 245, 246, and 247, respectively, and a light chain comprising CDR's L1, L2 and L3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 133 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 78, 79, and 80, respectively (as described in U.S. Patent Publication No. 20070110747).

The sclerostin binding agent may have a heavy chain comprising CDR's H1, H2, and H3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 145 or 392 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 245, 246, and 247, respectively, and a light chain comprising CDR's L1, L2, and L3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 141 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 78, 79, and 80, respectively (as described in U.S. Patent Publication No. 20070110747).

The sclerostin binding agent may have a heavy chain comprising CDR's H1, H2, and H3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 335 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 269, 270, and 271, respectively, and a light chain comprising CDR's L1, L2, and L3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 334 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 239, 240, and 241, respectively (as described in U.S. Patent Publication No. 20070110747).

Alternatively, the sclerostin binding agent has a heavy chain comprising CDR's H1, H2, and H3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 331 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 269, 270, and 271, respectively, and a light chain comprising CDR's L1, L2, and L3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 330 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 239, 240, and 241, respectively (as described in U.S. Patent Publication No. 20070110747).

The sclerostin binding agent may have a heavy chain comprising CDR's H1, H2, and H3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 345 or 396 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 269, 270, and 271, respectively, and a light chain comprising CDR's L1, L2, and L3 and comprising a polypeptide having the sequence provided in SEQ ID NO: 341 or a variant thereof in which said CDR's are at least 75% identical to SEQ ID NO: 239, 240, and 241, respectively (as described in U.S. Patent Publication No. 20070110747).

Alternatively, the sclerostin binding agent has a heavy chain comprising a polypeptide having the sequence provided in SEQ ID NO: 137, and a light chain comprising a polypeptide having the sequence provided in SEQ ID NO: 133; or a heavy chain comprising a polypeptide having the sequence provided in SEQ ID NO: 145 or 392, and a light chain comprising a polypeptide having the sequence provided in SEQ ID NO: 141; or a heavy chain comprising a polypeptide having the sequence provided in SEQ ID NO: 335, and a light chain comprising a polypeptide having the sequence provided in SEQ ID NO: 334; or a heavy chain comprising a polypeptide having the sequence provided in

SEQ ID NO: 331, and a light chain comprising a polypeptide having the sequence provided in SEQ ID NO: 330; or a heavy chain comprising a polypeptide having the sequence provided in SEQ ID NO: 345 or 396, and a light chain comprising a polypeptide having the sequence provided in SEQ ID NO: 341 (as described in U.S. Patent Publication No. 20070110747).

Sclerostin binding agents for use in the inventive method preferably modulate sclerostin function in the cell-based assay described in U.S. Patent Publication No. 20070110747 and/or the in vivo assay described in U.S. Patent Publication No. 20070110747 and/or bind to one or more of the epitopes described in U.S. Patent Publication No. 20070110747 and/or cross-block the binding of one of the antibodies described in U.S. Patent Publication No. 20070110747 and/or are cross-blocked from binding sclerostin by one of the antibodies described in U.S. Patent Publication No. 20070110747.

Alternatively, the inventive method can comprise administering a sclerostin inhibitor other than a sclerostin binding agent described herein. Such agents can act directly or indirectly on SOST or sclerostin. Sclerostin inhibitors contemplated for use in the inventive method include those described in U.S. Patent Publication No. 20030229041 (the entire disclosure of which is hereby incorporated by reference, with particular emphasis upon the description of sclerostin inhibitors). For example, agents useful for modulating SOST expression and sclerostin activity include, but are not limited to, steroids (such as those corresponding to Formula 1 of U.S. Patent Publication No. 20030229041), alkaloids, terpenoids, peptoids, and synthetic chemicals. In some embodiments, the SOST antagonist or agonist can bind to a glucocorticoid receptor. For example, dexamethasone tends to abolish the stimulatory effect of BMP-4 and BMP-6 on SOST expression. Other chemical entities including glucocorticoid analogs, bile salts (such as those corresponding to Formula 3 of U.S. Patent Publication No. 20030229041), and prostaglandins (such as those corresponding to Formula 2 of U.S. Patent Publication No. 20030229041) also modulate the effects of bone morphogenetic proteins on SOST expression, and are contemplated for use in the inventive method.

The sclerostin inhibitor may also be other small molecule therapeutics that act directly or indirectly on SOST or sclerostin to decrease the level of at least one bone resorative marker and/or increase the level of at least one bone formation marker in vivo. The term "small molecule" includes a compound or molecular complex, either synthetic, naturally derived, or partially synthetic, and which preferably has a molecular weight of less than 5,000 Daltons (e.g., between about 100 and 1,500 Daltons). Agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including spatially addressable parallel solid phase or solution phase libraries, synthetic library methods requiring deconvolution, the "one-bead one-compound" library method, and synthetic library methods using affinity chromatography selection (see, e.g., Lam, *Anticancer Drug Des.*, 12:145 (1997) and U.S. Pat. Nos. 5,738,996; 5,807,683; and 7,261,892). Methods of developing and screening sclerostin inhibitors are further described in U.S. Patent Publication No. 20030229041, the discussion of which is hereby incorporated by reference.

Sclerostin expression inhibitors that may be used according to the methods of the invention include inhibitor oligonucleotides or polynucleotides, including pharmaceutically acceptable salts thereof, e.g., sodium salts. Nonlimiting examples include: antisense oligonucleotides (Eckstein, *Antisense Nucleic Acid Drug Dev.*, 10: 117-121 (2000); Crooke, *Methods Enzymol.*, 313: 3-45 (2000); Guvakov et al., *J. Biol. Chem.*, 270: 2620-2627 (1995); Manoharan, *Biochim. Biophys. Acta*, 1489: 117-130 (1999); Baker et al., *J. Biol. Chem.*, 272: 11994-12000 (1997); Kurreck, *Eur. J. Biochem.*, 270: 1628-1644 (2003); Sierakowska et al., *Proc. Natl. Acad. Sci. USA*, 93: 12840-12844 (1996); Marwick, *J. Am. Med. Assoc.*, 280: 871 (1998); Tomita and Morishita, *Curr. Pharm. Des.*, 10: 797-803 (2004); Gleave and Monia, *Nat. Rev. Cancer*, 5: 468-479 (2005) and Patil, *AAPS J.*, 7: E61-E77 (2005)), triplex oligonucleotides (Francois et al., *Nucleic Acids Res.*, 16: 11431-11440 (1988) and Moser and Dervan, *Science*, 238: 645-650 (1987)), ribozymes/deoxyribozymes (DNAzymes) (Kruger et al., *Tetrahymena Cell*, 31: 147-157 (1982); Uhlenbeck, *Nature*, 328: 596-600 (1987); Sigurdsson and Eckstein, *Trends Biotechnol.*, 13: 286-289 (1995); Kumar et al., *Gene Ther.*, 12: 1486-1493 (2005); Breaker and Joyce, *Chem. Biol.*, 1: 223-229 (1994); Khachigian, *Curr. Pharm. Biotechnol.*, 5: 337-339 (2004); Khachigian, *Biochem. Pharmacol.*, 68: 1023-1025 (2004) and Trulzsch and Wood, *J. Neurochem.*, 88: 257-265 (2004)), small-interfering RNAs/RNAi (Fire et al., *Nature*, 391: 806-811 (1998); Montgomery et al., *Proc. Natl. Acad. Sci. U.S.A.*, 95: 15502-15507 (1998); Cullen, *Nat. Immunol.*, 3: 597-599 (2002); Hannon, *Nature*, 418: 244-251 (2002); Bernstein et al., *Nature*, 409: 363-366 (2001); Nykanen et al., *Cell*, 107: 309-321 (2001); Gilmore et al., *J. Drug Target.*, 12: 315-340 (2004); Reynolds et al., *Nat. Biotechnol.*, 22: 326-330 (2004); Soutschek et al., *Nature*, 432:173-178 (2004); Ralph et al., *Nat. Med.*, 11: 429-433 (2005); Xia et al., *Nat. Med.*, 10: 816-820 (2004) and Miller et al., *Nucleic Acids Res.*, 32: 661-668 (2004)), aptamers (Ellington and Szostak, *Nature*, 346: 818-822 (1990); Doudna et al., *Proc. Natl. Acad. Sci. U.S.A.*, 92: 2355-2359 (1995); Tuerk and Gold, *Science*, 249: 505-510 (1990); White et al., *Mol. Ther.*, 4: 567-573 (2001); Rusconi et al., *Nature*, 419: 90-94 (2002); Nimjee et al., *Mol. Ther.*, 14: 408-415 (2006); Gragoudas et al., *N. Engl. J. Med.*, 351: 3805-2816 (2004); Vinores, *Curr. Opin. Mol. Ther.*, 5673-679 (2003) and Kourlas and Schiller et al., *Clin. Ther.*, 28: 36-44 (2006)) or decoy oligonucleotides (Morishita et al., *Proc. Natl. Acad. Sci. U.S.A.*, 92: 5855-5859 (1995); Alexander et al., *J. Am. Med. Assoc.*, 294: 2446-2454 (2005); Mann and Dzau, *J. Clin. Invest.*, 106: 1071-1075 (2000) and Nimjee et al., *Annu. Rev. Med.*, 56: 555-583 (2005)). The foregoing documents are hereby incorporated by reference in their entirety herein, with particular emphasis on those sections of the documents relating to methods of designing, making and using inhibitory oligonucleotides. Commercial providers such as Ambion Inc. (Austin, Tex.), Dharmacon Inc. (Lafayette, Colo.), Invivogen (San Diego, Calif.), and Molecular Research Laboratories, LLC (Herndon, Va.) generate custom siRNA molecules. In addition, commercial kits are available to produce custom siRNA molecules, such as SILENCER™ siRNA Construction Kit (Ambion Inc., Austin, Tex.) or psiRNA System (Invivogen, San Diego, Calif.).

Inhibitory oligonucleotides which are stable, have a high resistance to nucleases, possess suitable pharmacokinetics to allow them to traffic to target tissue site at non-toxic doses, and have the ability to cross through plasma membranes are contemplated for use as a therapeutic. Inhibitory oligonucleotides may be complementary to the coding portion of a target gene, 3' or 5' untranslated regions, or intronic sequences in a gene, or alternatively coding or intron sequences in the target mRNA. Intron sequences are generally less conserved and thus may provide greater specificity. In one embodiment, the inhibitory oligonucleotide inhibits expression of a gene product of one species but not its homologue in another species; in

other embodiments, the inhibitory oligonucleotide inhibits expression of a gene in two species, e.g. human and primate, or human and murine.

The constitutive expression of antisense oligonucleotides in cells has been shown to inhibit gene expression, possibly via the blockage of translation or prevention of splicing. In certain embodiments, the inhibitory oligonucleotide is capable of hybridizing to at least 8, 9, 10, 11, or 12 consecutive bases of the sclerostin gene or mRNA (or the reverse strand thereof) under moderate or high stringency conditions. Suitable inhibitory oligonucleotides may be single stranded and contain a segment, e.g. at least 12, 15 or 18 bases in length, that is sufficiently complementary to, and specific for, an mRNA or DNA molecule such that it hybridizes to the mRNA or DNA molecule and inhibits transcription, splicing or translation. Generally complementarity over a length of less than 30 bases is more than sufficient.

Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C. for short nucleic acids (e.g., 10 to 50 nucleotides) and at least about 60° C. for longer nucleic acids (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30% to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulphate) at 37° C., and a wash in 1× to 2×SSC (20×SSC=3.0 M NaCl/0.3 M trisodium citrate) at 50° C. to 55° C. Exemplary moderate stringency conditions include hybridization in 40% to 45% formamide, 1.0 M NaCl, 1% SDS at 37° C., and a wash in 0.5× to 1×SSC at 55° C. to 60° C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37° C., and a wash in 0.1×SSC at 60° C. to 65° C. Duration of hybridization is generally less than about 24 hours, usually about 4 hours to about 12 hours.

In some cases, depending on the length of the complementary region, one, two or more mismatches may be tolerated without affecting inhibitory function. In certain embodiments, the inhibitory oligonucleotide is an antisense oligonucleotide, an inhibitory RNA (including siRNA or RNAi, or shRNA), a DNA enzyme, a ribozyme (optionally a hammerhead ribozyme), an aptamer, or pharmaceutically acceptable salts thereof. In one embodiment, the oligonucleotide is complementary to at least 10 bases of the nucleotide sequence encoding SEQ ID NO: 1 of U.S. Patent Publication No. 20040158045. In one embodiment, the oligonucleotide targets the nucleotides located in the vicinity of the 3' untranslated region of the sclerostin mRNA.

The specific sequence utilized in design of the oligonucleotides may be any contiguous sequence of nucleotides contained within the expressed gene message of the target. Factors that govern a target site for the inhibitory oligonucleotide sequence include the length of the oligonucleotide, binding affinity, and accessibility of the target sequence. Sequences may be screened in vitro for potency of their inhibitory activity by measuring inhibition of target protein translation and target related phenotype, e.g., inhibition of cell proliferation in cells in culture. In general it is known that most regions of the RNA (5' and 3' untranslated regions, AUG initiation, coding, splice junctions and introns) can be targeted using antisense oligonucleotides. Programs and algorithms, known in the art, may be used to select appropriate target sequences. In addition, optimal sequences may be selected utilizing programs designed to predict the secondary structure of a specified single stranded nucleic acid sequence and allowing selec-

tion of those sequences likely to occur in exposed single stranded regions of a folded mRNA. Methods and compositions for designing appropriate oligonucleotides may be found, for example, in U.S. Pat. No. 6,251,588, the contents of which are incorporated herein by reference in its entirety.

Phosphorothioate antisense oligonucleotides may be used. Modifications of the phosphodiester linkage as well as of the heterocycle or the sugar may provide an increase in efficiency. Phosphorothioate is used to modify the phosphodiester linkage. An N3'-P5' phosphoramidate linkage has been described as stabilizing oligonucleotides to nucleases and increasing the binding to RNA. Peptide nucleic acid (PNA) linkage is a complete replacement of the ribose and phosphodiester backbone and is stable to nucleases, increases the binding affinity to RNA, and does not allow cleavage by RNase H. Its basic structure is also amenable to modifications that may allow its optimization as an antisense component. With respect to modifications of the heterocycle, certain heterocycle modifications have proven to augment antisense effects without interfering with RNase H activity. An example of such modification is C-5 thiazole modification. Finally, modification of the sugar may also be considered. 2'-O-propyl and 2'-methoxyethoxy ribose modifications stabilize oligonucleotides to nucleases in cell culture and *in vivo*.

Most mRNAs have been shown to contain a number of secondary and tertiary structures. Secondary structural elements in RNA are formed largely by Watson-Crick type interactions between different regions of the same RNA molecule. Important secondary structural elements include intramolecular double stranded regions, hairpin loops, bulges in duplex RNA and internal loops. Tertiary structural elements are formed when secondary structural elements come in contact with each other or with single stranded regions to produce a more complex three dimensional structure. A number of researchers have measured the binding energies of a large number of RNA duplex structures and have derived a set of rules which can be used to predict the secondary structure of RNA (see, e.g., Jaeger et al., *Proc. Natl. Acad. Sci. USA*, 86:7706 (1989); and Turner et al., *Annu. Rev. Biophys. Bioophys. Chem.* 17:167 (1988)). The rules are useful in identification of RNA structural elements and, in particular, for identifying single stranded RNA regions which may represent segments of the mRNA to target for siRNA, ribozyme, or antisense technologies.

Short interfering (si) RNA technology (also known as RNAi) generally involves degradation of an mRNA of a particular sequence induced by double-stranded RNA (dsRNA) that is homologous to that sequence, thereby "interfering" with expression of the corresponding gene. Any selected gene may be repressed by introducing a dsRNA which corresponds to all or a substantial part of the mRNA for that gene. It appears that when a long dsRNA is expressed, it is initially processed by a ribonuclease III into shorter dsRNA oligonucleotides of as few as 21 to 22 base pairs in length. Accordingly, siRNA may be affected by introduction or expression of relatively short homologous dsRNAs. Exemplary siRNAs have sense and antisense strands of about 21 nucleotides that form approximately 19 nucleotides of double stranded RNA with overhangs of two nucleotides at each 3' end. Indeed the use of relatively short homologous dsRNAs may have certain advantages.

Mammalian cells have at least two pathways that are affected by double-stranded RNA (dsRNA). In the sequence-specific siRNA pathway, the initiating dsRNA is first broken into short interfering RNAs, as described above. Short interfering RNAs are thought to provide the sequence information that allows a specific messenger RNA to be targeted for

degradation. In contrast, the nonspecific pathway is triggered by dsRNA of any sequence, as long as it is at least about 30 base pairs in length.

The nonspecific effects occur because dsRNA activates two enzymes: PKR, which in its active form phosphorylates the translation initiation factor eIF2 to shut down all protein synthesis, and 2', 5' oligoadenylate synthetase (2',5'-AS), which synthesizes a molecule that activates RNase L, a nonspecific enzyme that targets all mRNAs. The nonspecific pathway may represent a host response to stress or viral infection, and, in general, the effects of the nonspecific pathway are preferably minimized. Significantly, longer dsRNAs appear to be required to induce the nonspecific pathway and, accordingly, dsRNAs shorter than about 30 bases pairs are contemplated to effect gene repression by RNAi (see Hunter et al., *J. Biol. Chem.*, 250: 409-17 (1975); Manche et al., *Mol. Cell. Biol.* 12: 5239-48 (1992); Minks et al., *J. Biol. Chem.*, 254: 10180-3 (1979); and Elbashir et al., *Nature*, 411: 494-8 (2001)).

siRNA has proven to be an effective means of decreasing gene expression in a variety of cell types. siRNA typically decreases expression of a gene to lower levels than that achieved using antisense techniques, and frequently eliminates expression entirely (see Bass, *Nature*, 411: 428-9 (2001)). In mammalian cells, siRNAs are effective at concentrations that are several orders of magnitude below the concentrations typically used in antisense experiments (Elbashir et al., *Nature*, 411:494-8 (2001)).

The double stranded oligonucleotides used to effect RNAi are preferably less than 30 base pairs in length, for example, about 25, 24, 23, 22, 21, 20, 19, 18, or 17 base pairs or less in length, and contain a segment sufficiently complementary to the target mRNA to allow hybridization to the target mRNA. Optionally the dsRNA oligonucleotides may include 3' overhang ends. Exemplary 2-nucleotide 3' overhangs may be composed of ribonucleotide residues of any type and may even be composed of 2'-deoxythymidine residues, which lowers the cost of RNA synthesis and may enhance nuclease resistance of siRNAs in the cell culture medium and within transfected cells (see Elbashi et al., supra). Exemplary dsRNAs may be synthesized chemically or produced in vitro or in vivo using appropriate expression vectors (see, e.g., Elbashir et al., *Genes Dev.*, 15:188-200 (2001)). Longer RNAs may be transcribed from promoters, such as T7 RNA polymerase promoters, known in the art.

Longer dsRNAs of 50, 75, 100, or even 500 base pairs or more also may be utilized in certain embodiments of the invention. Exemplary concentrations of dsRNAs for effecting RNAi are about 0.05 nM, 0.1 nM, 0.5 nM, 1.0 nM, 1.5 nM, 25 nM, or 100 nM, although other concentrations may be utilized depending upon the nature of the cells treated, the gene target and other factors readily discernable to the skilled artisan.

Further compositions, methods and applications of siRNA technology are provided in U.S. Pat. Nos. 6,278,039; 5,723,750; and 5,244,805, which are incorporated herein by reference in its entirety.

Compared to siRNA, shRNA offers advantages in silencing longevity and delivery options. See, e.g., Hannon et al., *Nature*, 431:371-378 (2004) for review. Vectors that produce shRNAs, which are processed intracellularly into short duplex RNAs having siRNA-like properties have been reported (Brummelkamp et al., *Science*, 296: 550-553 (2000); Paddison et al., *Genes Dev.*, 16: 948-958 (2002)). Such vectors provide a renewable source of a gene-silencing reagent that can mediate persistent gene silencing after stable integration of the vector into the host-cell genome. Further-

more, the core silencing 'hairpin' cassette can be readily inserted into retroviral, lentiviral, or adenoviral vectors, facilitating delivery of shRNAs into a broad range of cell types (Brummelkamp et al., *Cancer Cell*, 2:243-247 (2002); Dirac et al., *J. Biol. Chem.*, 278:11731-11734 (2003); Michiels et al., *Nat. Biotechnol.*, 20:1154-1157 (2002); Stegmeier et al., *Proc. Natl. Acad. Sci. USA*, 102:13212-13217 (2005); Khvorova et al., *Cell*, 115:209-216 (2003)) in any of the innumerable ways that have been devised for delivery of DNA constructs that allow ectopic mRNA expression.

A hairpin can be organized in either a left-handed hairpin (i.e., 5'-antisense-loop-sense-3') or a right-handed hairpin (i.e., 5'-sense-loop-antisense-3'). The siRNA may also contain overhangs at either the 5' or 3' end of either the sense strand or the antisense strand, depending upon the organization of the hairpin. Preferably, if there are any overhangs, they are on the 3' end of the hairpin and comprise between 1 to 6 bases. The overhangs can be unmodified, or can contain one or more specificity or stabilizing modifications, such as a halogen or O-alkyl modification of the 2' position, or internucleotide modifications such as phosphorothioate, phosphorodithioate, or methylphosphonate modifications. The overhangs can be ribonucleic acid, deoxyribonucleic acid, or a combination of ribonucleic acid and deoxyribonucleic acid.

Additionally, a hairpin can further comprise a phosphate group on the 5'-most nucleotide. The phosphorylation of the 5'-most nucleotide refers to the presence of one or more phosphate groups attached to the 5' carbon of the sugar moiety of the 5'-terminal nucleotide. Preferably, there is only one phosphate group on the 5' end of the region that will form the antisense strand following Dicer processing. In one exemplary embodiment, a right-handed hairpin can include a 5' end (i.e., the free 5' end of the sense region) that does not have a 5' phosphate group, or can have the 5' carbon of the free 5'-most nucleotide of the sense region being modified in such a way that prevents phosphorylation. This can be achieved by a variety of methods including, but not limited to, addition of a phosphorylation blocking group (e.g., a 5'-O-alkyl group), or elimination of the 5'-OH functional group (e.g., the 5'-most nucleotide is a 5'-deoxy nucleotide). In cases where the hairpin is a left-handed hairpin, preferably the 5' carbon position of the 5'-most nucleotide is phosphorylated.

Hairpins that have stem lengths longer than 26 base pairs can be processed by Dicer such that some portions are not part of the resulting siRNA that facilitates mRNA degradation. Accordingly the first region, which may comprise sense nucleotides, and the second region, which may comprise antisense nucleotides, may also contain a stretch of nucleotides that are complementary (or at least substantially complementary to each other), but are or are not the same as or complementary to the target mRNA. While the stem of the shRNA can be composed of complementary or partially complementary antisense and sense strands exclusive of overhangs, the shRNA can also include the following: (1) the portion of the molecule that is distal to the eventual Dicer cut site contains a region that is substantially complementary/homologous to the target mRNA; and (2) the region of the stem that is proximal to the Dicer cut site (i.e., the region adjacent to the loop) is unrelated or only partially related (e.g., complementary/homologous) to the target mRNA. The nucleotide content of this second region can be chosen based on a number of parameters including but not limited to thermodynamic traits or profiles.

Modified shRNAs can retain the modifications in the post-Dicer processed duplex. In exemplary embodiments, in cases in which the hairpin is a right handed hairpin (e.g., 5'-S-loop-AS-3') containing 2-6 nucleotide overhangs on the 3' end of

the molecule, 2'-O-methyl modifications can be added to nucleotides at position 2, positions 1 and 2, or positions 1, 2, and 3 at the 5' end of the hairpin. Also, Dicer processing of hairpins with this configuration can retain the 5' end of the sense strand intact, thus preserving the pattern of chemical modification in the post-Dicer processed duplex. Presence of a 3' overhang in this configuration can be particularly advantageous since blunt ended molecules containing the prescribed modification pattern can be further processed by Dicer in such a way that the nucleotides carrying the 2' modifications are removed. In cases where the 3' overhang is present/retained, the resulting duplex carrying the sense-modified nucleotides can have highly favorable traits with respect to silencing specificity and functionality. Examples of exemplary modification patterns are described in detail in U.S. Patent Publication No. 20050223427 and International Patent Publication Nos. WO 2004/090105 and WO 2005/078094, the disclosures of each of which are incorporated by reference herein in their entirety.

shRNA may comprise sequences that were selected at random, or according to any rational design selection procedure. For example, rational design algorithms are described in International Patent Publication No. WO 2004/045543 and U.S. Patent Publication No. 20050255487, the disclosures of which are incorporated herein by reference in their entireties. Additionally, it may be desirable to select sequences in whole or in part based on average internal stability profiles ("AISPs") or regional internal stability profiles ("RISPs") that may facilitate access or processing by cellular machinery.

Ribozymes are enzymatic RNA molecules capable of catalyzing specific cleavage of mRNA, thus preventing translation. (For a review, see Rossi, *Current Biology*, 4:469-471 (1994)). The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme molecule to complementary target RNA, followed by an endonucleolytic cleavage event. The ribozyme molecules preferably include (1) one or more sequences complementary to a target mRNA, and (2) the well known catalytic sequence responsible for mRNA cleavage or a functionally equivalent sequence (see, e.g., U.S. Pat. No. 5,093,246, which is incorporated herein by reference in its entirety).

While ribozymes that cleave mRNA at site-specific recognition sequences can be used to destroy target mRNAs, hammerhead ribozymes may alternatively be used. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. Preferably, the target mRNA has the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, *Nature*, 334:585-591 (1988); and International Patent Publication No. WO 89/05852, the contents of which are incorporated herein by reference in its entirety.

Gene targeting ribozymes may contain a hybridizing region complementary to two regions of a target mRNA, each of which is at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleotides (but which need not both be the same length).

Hammerhead ribozyme sequences can be embedded in a stable RNA such as a transfer RNA (tRNA) to increase cleavage efficiency in vivo (Perriman et al., *Proc. Natl. Acad. Sci. USA*, 92:6175-79 (1995); de Feyter and Gaudron, *Methods in Molecular Biology*, Vol. 74, Chapter 43, "Expressing Ribozymes in Plants," Turner, P. C. (ed.), Humana Press Inc., Totowa, N.J.). In particular, RNA polymerase III-mediated expression of tRNA fusion ribozymes are well known in the art (see Kawasaki et al., *Nature*, 393:284-9 (1998); Kuwabara

et al., *Nature Biotechnol.*, 16:961-5 (1998); and Kuwabara et al., *Mol. Cell*, 2:617-27 (1998); Koseki et al., *J. Virol.*, 73:1868-77 (1999); Kuwabara et al., *Proc. Natl. Acad. Sci. USA*, 96:1886-91 (1999); Tanabe et al., *Nature*, 406:473-4 (2000)). There are typically a number of potential hammerhead ribozyme cleavage sites within a given target cDNA sequence. Preferably the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the target mRNA to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts. Furthermore, the use of any cleavage recognition site located in the target sequence encoding different portions of the target mRNA would allow the selective targeting of one or the other target genes.

Ribozymes for use in the inventive method also include RNA endoribonucleases ("Cech-type ribozymes") such as the one which occurs naturally in *Tetrahymena thermophila* (known as the IVS, or L-19 IVS RNA) and which has been extensively described in Zaug et al., *Science*, 224:574-578 (1984); Zaug, et al., *Science*, 231:470-475 (1986); Zaug et al., *Nature*, 324:429-433 (1986); International Patent Publication No. WO 88/04300; and Been et al., *Cell*, 47:207-216 (1986)). The Cech-type ribozymes have an eight base pair active site which hybridizes to a target RNA sequence whereafter cleavage of the target RNA takes place. In one embodiment, the inventive method employs those Cech-type ribozymes which target eight base-pair active site sequences that are present in a target gene or nucleic acid sequence.

Ribozymes can be composed of modified oligonucleotides (e.g., for improved stability, targeting, etc.) and can be chemically synthesized or produced through an expression vector. Because ribozymes, unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency. Additionally, in certain embodiments, a ribozyme may be designed by first identifying a sequence portion sufficient to cause effective knockdown by RNAi. Portions of the same sequence may then be incorporated into a ribozyme.

Alternatively, target gene expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of the gene (i.e., the promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells in the body. (See generally Helene, C., *Anticancer Drug Des.*, 6:569-84 (1991); Helene et al., *Ann. N.Y. Acad. Sci.*, 660:27-36 (1992); and Maher, L. J., *Bioassays*, 14:807-15 (1992)).

Nucleic acid molecules to be used in triple helix formation for the inhibition of transcription are preferably single stranded and composed of deoxyribonucleotides. The base composition of these oligonucleotides should promote triple helix formation via Hoogsteen base pairing rules, which generally require sizable stretches of either purines or pyrimidines to be present on one strand of a duplex. Nucleotide sequences may be pyrimidine-based, which will result in TAT and CGC triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules provide base complementarity to a purine-rich region of a single strand of the duplex in a parallel orientation to that strand. In addition, nucleic acid molecules may be chosen that are purine-rich, for example, containing a stretch of G residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are located on a single strand of the targeted duplex, resulting in CGC triplets across the three strands in the triplex.

Alternatively, the target sequences that can be targeted for triple helix formation may be increased by creating a so-called "switchback" nucleic acid molecule. Switchback mol-

ecules are synthesized in an alternating 5'-3',3'-5' manner, such that they base pair with first one strand of a duplex and then the other, eliminating the necessity for a sizable stretch of either purines or pyrimidines to be present on one strand of a duplex.

Alternatively, DNA enzymes may be used to inhibit expression of target gene, such as the sclerostin gene. DNA enzymes incorporate some of the mechanistic features of both antisense and ribozyme technologies. DNA enzymes are designed so that they recognize a particular target nucleic acid sequence, much like an antisense oligonucleotide. They are, however, also catalytic and specifically cleave the target nucleic acid.

DNA enzymes include two basic types identified by Santoro and Joyce (see, for example, U.S. Pat. No. 6,110,462). The 10-23 DNA enzyme comprises a loop structure which connects two arms. The two arms provide specificity by recognizing the particular target nucleic acid sequence while the loop structure provides catalytic function under physiological conditions.

Preferably, the unique or substantially unique sequence is a G/C rich segment of approximately 18 to 22 nucleotides. High G/C content helps insure a stronger interaction between the DNA enzyme and the target sequence. The specific antisense recognition sequence that will target the enzyme to the message may be divided between the two arms of the DNA enzyme.

Methods of making and administering DNA enzymes can be found, for example, in U.S. Pat. No. 6,110,462. Additionally, one of skill in the art will recognize that, like antisense oligonucleotide, DNA enzymes can be optionally modified to improve stability and improve resistance to degradation.

Inhibitory oligonucleotides can be administered directly or delivered to cells by transformation or transfection via a vector, including viral vectors or plasmids, into which has been placed DNA encoding the inhibitory oligonucleotide with the appropriate regulatory sequences, including a promoter, to result in expression of the inhibitory oligonucleotide in the desired cell. Known methods include standard transient transfection, stable transfection and delivery using viruses ranging from retroviruses to adenoviruses. Delivery of nucleic acid inhibitors by replicating or replication-deficient vectors is contemplated. Expression can also be driven by either constitutive or inducible promoter systems (Paddison et al., *Methods Mol. Biol.*, 265:85-100 (2004)). In other embodiments, expression may be under the control of tissue or development-specific promoters.

For example, vectors may be introduced by transfection using carrier compositions such as Lipofectamine 2000 (Life Technologies) or Oligofectamine (Life Technologies). Transfection efficiency may be checked using fluorescence microscopy for mammalian cell lines after co-transfection of hGFP-encoding pAD3 (Kehlenback et al., *J. Cell Biol.*, 141:863-74 (1998)).

The delivery route will be the one that provides the best inhibitory effect as measured according to the criteria described above. Delivery mediated by cationic liposomes, delivery by retroviral vectors and direct delivery are efficient.

The effectiveness of the inhibitory oligonucleotide may be assessed by any of a number of assays, including reverse transcriptase polymerase chain reaction or Northern blot analysis to determine the level of existing human sclerostin mRNA, or Western blot analysis using antibodies which recognize the human sclerostin protein, after sufficient time for turnover of the endogenous pool after new protein synthesis is repressed.

The invention is further described in the following example. The example serves only to illustrate the invention and are not intended to limit the scope of the invention in any way.

5

EXAMPLE

This example describes in vivo studies wherein a sclerostin binding agent reduced the level of a marker of bone resorption and increased the level of one or more markers of bone formation.

A single-center, randomized, double-blind, placebo-controlled, ascending single-dose study in healthy men and postmenopausal women was conducted. Approximately 72 subjects enrolled in one of six dose cohorts. For cohorts 1, 2, 3a, 4, 5 and 6a, eight healthy postmenopausal women were randomized to receive a sclerostin binding agent or placebo via subcutaneous injection in a 3:1 ratio at dose levels of 0.1 mg/kg, 0.3 mg/kg, 1 mg/kg, 3 mg/kg, 5 mg/kg, or 10 mg/kg, respectively. In cohorts 3b and 6b, 8 healthy males received the sclerostin binding agent or a placebo intravenously and subcutaneously in a 3:3:1:1 ratio (sclerostin binding agent intravenously:sclerostin binding agent subcutaneously:placebo intravenously:placebo subcutaneously) at a dose level of 1 mg/kg or 10 mg/kg (reduced to 5 mg/kg), respectively. For cohorts 3c and 6c, four healthy postmenopausal women were randomized to receive the sclerostin binding agent or placebo intravenously in a 3:1 ratio at a dose level of 1 mg/kg or 10 mg/kg (reduced to 5 mg/kg), respectively.

The anti-sclerostin therapy was monitored by measuring the levels of bone resorption markers and bone formation markers prior to administration, then at least every week for 12 weeks post-administration. P1NP and BSAP levels were monitored following a single-dose subcutaneous administration of sclerostin binding agent in healthy, postmenopausal women (see FIGS. 1 and 2). Subjects dosed at 0.1 mg/kg and 0.3 mg/kg enjoyed the least elevation of P1NP or BSAP levels (e.g., levels increased less than 20%).

P1NP levels in subjects given 1 mg/kg increased approximately 20% by Day 10 and gradually tapered off to baseline around Day 56, while BSAP levels peaked at Day 14 at about 30% above baseline. P1NP and BSAP levels in subjects given 3 mg/kg peaked at Day 21 at approximately 100% (P1NP) and 60% (BSAP) increase from baseline, and returned to baseline about Day 56. In subjects administered 5 mg/kg, the level of P1NP rose to about 140% above baseline at Day 14 post-administration, and remained elevated at Day 77. In other words, the level of P1NP increased about 140% by two weeks post-treatment. BSAP rose to about 115% above baseline and remained elevated at Day 84. Similarly, administration of 10 mg/kg triggered a 180% increase in P1NP levels at about Day 28. P1NP levels remained elevated throughout the monitoring period. Subjects administered 10 mg/kg demonstrated a peak increase of BSAP levels at Day 21 (125% baseline for 3 weeks post-administration), which also remained elevated at Day 84. The results of the study are illustrated in FIGS. 1 and 2.

Osteocalcin also was monitored following a single-dose, subcutaneous administration of sclerostin binding agent in healthy, postmenopausal women (see FIG. 3). Subjects given less than 1 mg/kg experienced little elevation of Osteocalcin. Osteocalcin levels fluctuated in patients administered 1 mg/kg, peaking at about 30% above baseline at Days 21 and 35. Osteocalcin levels peaked at about 100% above baseline at Day 21 in subjects administered 3 mg/kg, and levels remained elevated until about Day 56. Likewise, administration of 5 mg/kg sclerostin binding agent resulted in a 140%

increase in osteocalcin levels at day 28, which levels remained at Day 84. Subjects dosed at 10 mg/kg demonstrated a peak osteocalcin level of about 180% above baseline at Day 35. Osteocalcin levels remained elevated above baseline until at least about Day 77.

Levels of the bone resorptive marker sCTX also were monitored (see FIG. 4). Subjects administered placebo and 0.1 mg/kg demonstrated modest decreases in sCTX levels (e.g., less than 20%). Administration of 0.3 mg/kg of sclerostin binding agent reduced sCTX levels by about 20% by Day 21 (i.e., sCTX levels were reduced about 20% by two weeks after treatment). Levels fluctuated in subjects dosed at 1 mg/kg but reached about 30% below baseline at Days 10, 28, and 49. Levels in subjects administered 3 mg/kg, 5 mg/kg, and 10 mg/kg fell lowest at Day 14 to about 35%, 55%, and 55% below baseline, respectively, and levels remained below baseline when monitored thereafter. A comparison of the levels of all monitored biomarkers is provided in FIG. 5.

Serum ionized calcium levels were monitored following a single, subcutaneous dose of sclerostin binding agent in healthy, postmenopausal women (see FIG. 6). Remarkably, ionized calcium levels did not fluctuate dramatically at any dosage. Indeed, all subjects (including those receiving placebo) experienced a modest transient decrease in serum ionized calcium of approximately 5% during the monitoring period.

Finally, bone mineral density was measured in the spine and hip of healthy, postmenopausal women receiving 1 mg/kg, 3 mg/kg, 5 mg/kg, or 10 mg/kg sclerostin binding

agent (see FIG. 7). Significant increases in BMD were observed in the spine, for example, at Days 28, 56, and 84, particularly in patients receiving 5 mg/kg and 10 mg/kg. BMD in the hip increased less than that of the spine, but BMD was elevated at Day 56 in patients administered 3 mg/kg, 5 mg/kg, and 10 mg/kg. BMD was further elevated at Day 84 in patients dosed at 5 mg/kg and 10 mg/kg.

This example illustrates the ability of the inventive method to reduce levels of a marker of bone resorption, elevate levels of markers of bone formation, and increase bone mineral density without dramatic alterations in serum calcium. The therapeutic effect of a single dose of sclerostin binding agent is long-lived, with increased bone formation marker levels and decreased bone resorptive marker levels continuing to be observed at 84 days (12 weeks) post treatment. Furthermore, data described herein suggests that the therapeutic efficacy of the invention have significant advantages compared to other treatments by “uncoupling” bone formation and bone resorption to maximize bone formation and mineralization *in vivo*.

20 All of the references cited herein, including patents, patent applications, literature publications, and the like, are hereby incorporated in their entireties by reference.

While this invention has been described with an emphasis upon preferred embodiments, it will be obvious to those of ordinary skill in the art that variations of the preferred compounds and methods may be used and that it is intended that the invention may be practiced otherwise than as specifically described herein. Accordingly, this invention includes all modifications encompassed within the spirit and scope of the invention as defined by the following claims.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 396

<210> SEQ ID NO 1
<211> LENGTH: 190
<212> TYPE: PRT
<213> ORGANISM: *Homo sapiens*

<400> SEQUENCE: 1

Leu Gly Glu Tyr Pro Glu Pro Pro Pro Glu Leu Glu Asn Asn Lys Thr
 20 25 30

Met Asn Arg Ala Glu Asn Gly Gly Arg Pro Pro His His Pro Phe Glu
35 40 45

Thr Lys Asp Val Ser Glu Tyr Ser Cys Arg Glu Leu His Phe Thr Arg
50 55 60

Tyr Val Thr Asp Gly Pro Cys Arg Ser Ala Lys Pro Val Thr Glu Leu
65 70 75 80

Val Cys Ser Gly Gln Cys Gly Pro Ala Arg Leu Leu Pro Asn Ala Ile
85 90 95

Gly Arg Gly Lys Trp Trp Arg Pro Ser Gly Pro Asp Phe Arg Cys Ile
100 105 110

Pro Asp Arg Tyr Arg Ala Gln Arg Val Gln Leu Leu Cys Pro Gly Gly
115 120 125

Glu Ala Pro Arg Ala Arg Lys Val Arg Leu Val Ala Ser Cys Lys Cys
130 135 140

Lys Arg Leu Thr Arg Phe His Asn Gln Ser Glu Leu Lys Asp Phe Gly
145 150 155 160

Thr Glu Ala Ala Arg Pro Gln Lys Gly Arg Lys Pro Arg Pro Arg Ala

-continued

| | | |
|-----|-----|-----|
| 165 | 170 | 175 |
|-----|-----|-----|

| | | |
|---|-----|-----|
| Arg Ser Ala Lys Ala Asn Gln Ala Glu Leu Glu Asn Ala Tyr | | |
| 180 | 185 | 190 |

<210> SEQ ID NO 2
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 2

| | | |
|---|---|----|
| Asp Val Ser Glu Tyr Ser Cys Arg Glu Leu His Phe Thr Arg | | |
| 1 | 5 | 10 |

<210> SEQ ID NO 3
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

| | | |
|---|---|----|
| Ser Ala Lys Pro Val Thr Glu Leu Val Cys Ser Gly Gln Cys Gly Pro | | |
| 1 | 5 | 10 |
| | | 15 |

<210> SEQ ID NO 4
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

| | | |
|---|---|----|
| Trp Trp Arg Pro Ser Gly Pro Asp Phe Arg Cys Ile Pro Asp Arg Tyr | | |
| 1 | 5 | 10 |
| | | 15 |

<210> SEQ ID NO 5
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

| | | |
|---|---|----|
| Leu Val Ala Ser Cys Lys Cys Lys Arg Leu Thr Arg | | |
| 1 | 5 | 10 |

<210> SEQ ID NO 6
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

| | | |
|---|---|----|
| Cys Gly Pro Ala Arg Leu Leu Pro Asn Ala Ile Gly Arg Gly Lys Trp | | |
| 1 | 5 | 10 |
| | | 15 |

| | | |
|---|----|--|
| Trp Arg Pro Ser Gly Pro Asp Phe Arg Cys | | |
| 20 | 25 | |

<210> SEQ ID NO 7
<211> LENGTH: 214
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 7

| | | |
|---|---|----|
| Asp Val Gln Met Ile Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly | | |
| 1 | 5 | 10 |
| | | 15 |

| | | |
|---|----|----|
| Asp Ile Val Thr Met Thr Cys Gln Ala Ser Gln Gly Thr Ser Ile Asn | | |
| 20 | 25 | 30 |

| | | |
|---|----|----|
| Leu Asn Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile | | |
| 35 | 40 | 45 |

-continued

Tyr Gly Ser Ser Asn Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Arg Tyr Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Asp
 65 70 75 80

Glu Asp Leu Ala Thr Tyr Phe Cys Leu Gln His Ser Tyr Leu Pro Tyr
 85 90 95

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala
 100 105 110

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
 115 120 125

Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
 130 135 140

Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
 145 150 155 160

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
 165 170 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
 180 185 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
 195 200 205

Phe Asn Arg Asn Glu Cys
 210

<210> SEQ ID NO 8
<211> LENGTH: 645
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 8

gatgtccaga tgattcagtc tccatcctcc ctgtctgcat ctttggaga catagtcacc 60
 atgacttgcc aggcaagtca gggcactagc attaatttaa actgggttca gcaaaaacca 120
 gggaggctc ctaagtcct gatctatggt tcaagcaact tggaagatgg ggtccatca 180
 aggttcagtg gcagtagata tggcagat ttcaactctca ccatcagcag cctggaggat 240
 gaagatctgg caacttattt ctgtctacaa catagtttac tcccgtacac gttcgagg 300
 gggaccaagc tggaaataaa acgggctgtat gctgcaccaa ctgttatccat cttccacca 360
 tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gttcttgaa caacttctac 420
 cccaaagaca tcaatgtcaa gtgaaagatt gatggcagt aacgacaaaa tggcgtctg 480
 aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcact 540
 ttgaccaagg acgagttatga acgacataac agtataccat gtgaggccac tcacaagaca 600
 tcaacttcac ccattgtcaa gagttcaac aggaatgagt gttag 645

<210> SEQ ID NO 9
<211> LENGTH: 236
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 9

Met Asn Thr Arg Ala Pro Ala Glu Phe Leu Gly Phe Leu Leu Trp
 1 5 10 15

Phe Leu Gly Ala Arg Cys Asp Val Gln Met Ile Gln Ser Pro Ser Ser
 20 25 30

Leu Ser Ala Ser Leu Gly Asp Ile Val Thr Met Thr Cys Gln Ala Ser

-continued

| 35 | 40 | 45 | |
|-----|-----|---|-----|
| Gln | Gly | Thr Ser Ile Asn Leu Asn Trp Phe Gln Gln Lys Pro Gly Lys | |
| 50 | 55 | 60 | |
| Ala | Pro | Lys Leu Leu Ile Tyr Gly Ser Ser Asn Leu Glu Asp Gly Val | |
| 65 | 70 | 75 | 80 |
| Pro | Ser | Arg Phe Ser Gly Ser Arg Tyr Gly Thr Asp Phe Thr Leu Thr | |
| 85 | 90 | 95 | |
| Ile | Ser | Ser Leu Glu Asp Glu Asp Leu Ala Thr Tyr Phe Cys Leu Gln | |
| 100 | 105 | 110 | |
| His | Ser | Tyr Leu Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile | |
| 115 | 120 | 125 | |
| Lys | Arg | Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser | |
| 130 | 135 | 140 | |
| Glu | Gln | Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn | |
| 145 | 150 | 155 | 160 |
| Phe | Tyr | Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu | |
| 165 | 170 | 175 | |
| Arg | Gln | Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp | |
| 180 | 185 | 190 | |
| Ser | Thr | Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr | |
| 195 | 200 | 205 | |
| Glu | Arg | His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr | |
| 210 | 215 | 220 | |
| Ser | Pro | Ile Val Lys Ser Phe Asn Arg Asn Glu Cys | |
| 225 | 230 | 235 | |

<210> SEQ_ID NO 10
 <211> LENGTH: 711
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 10

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agatgtatg tccagatgtat tcagtctcca tcctccctgt ctgcacatctt gggagacata     120
gtcaccatga cttgccaggc aagtcaaggc actagcatta atttaactg gtttcagcaa      180
aaaccaggga aggctctaa gctctgtat tatggttcaa gcaacttggc agatgggtc      240
ccatcaaggt tcagtgccag tagatatggg acagattca ctctcaccat cagcagcctg     300
gaggatgaag atctggcaac ttatctgtat ctacaacata gttatctccc gtacacgttc     360
ggagggggga ccaagctgga aataaaacgg gctgatgtcg caccaactgt atccatctc     420
ccaccatcca gtgagcgtt aacatctggc ggtgcctcag tcgtgtgcctt cttgaacaac     480
ttctacccca aagacatcaa tgtcaagtgg aagattgtat gcagtgaacg acaaaatggc     540
gtcctgaaca gttggactga tcaggacgc aaagacagca cctacagcat gagcagcacc     600
ctcacgttga ccaaggacga gttatggc cataacagct atacctgtga ggccactcac     660
aagacatcaa cttcacccat tgtcaagacg ttcaacaggg atgagtgtta g                711

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<210> SEQ_ID NO 11
 <211> LENGTH: 443
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 11

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Thr Pro Gly Ala

US 9,089,553 B2

35**36**

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| 1 | 5 | 10 | 15 |
|---|-----|-----|-----|
| Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His | | | |
| 20 | 25 | 30 | |
| Tyr Met Ser Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile | | | |
| 35 | 40 | 45 | |
| Gly Asp Ile Asn Pro Tyr Ser Gly Glu Thr Thr Tyr Asn Gln Lys Phe | | | |
| 50 | 55 | 60 | |
| Lys Gly Thr Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Ile Ala Tyr | | | |
| 65 | 70 | 75 | 80 |
| Met Glu Ile Arg Gly Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys | | | |
| 85 | 90 | 95 | |
| Ala Arg Asp Asp Tyr Asp Ala Ser Pro Phe Ala Tyr Trp Gly Gln Gly | | | |
| 100 | 105 | 110 | |
| Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser Val Tyr | | | |
| 115 | 120 | 125 | |
| Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu | | | |
| 130 | 135 | 140 | |
| Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp | | | |
| 145 | 150 | 155 | 160 |
| Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu | | | |
| 165 | 170 | 175 | |
| Gln Ser Asp Leu Tyr Thr Leu Ser Ser Val Thr Val Pro Ser Ser | | | |
| 180 | 185 | 190 | |
| Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser | | | |
| 195 | 200 | 205 | |
| Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys | | | |
| 210 | 215 | 220 | |
| Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro | | | |
| 225 | 230 | 235 | 240 |
| Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr | | | |
| 245 | 250 | 255 | |
| Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser | | | |
| 260 | 265 | 270 | |
| Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg | | | |
| 275 | 280 | 285 | |
| Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile | | | |
| 290 | 295 | 300 | |
| Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn | | | |
| 305 | 310 | 315 | 320 |
| Ser Pro Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys | | | |
| 325 | 330 | 335 | |
| Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu | | | |
| 340 | 345 | 350 | |
| Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe | | | |
| 355 | 360 | 365 | |
| Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala | | | |
| 370 | 375 | 380 | |
| Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr | | | |
| 385 | 390 | 395 | 400 |
| Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly | | | |
| 405 | 410 | 415 | |
| Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His | | | |
| 420 | 425 | 430 | |

Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
435 440

<210> SEQ ID NO 12
<211> LENGTH: 1332
<212> TYPE: DNA
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 12

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tcttgttaagg cttcttgata cacattcaact gaccactaca tgagctgggt gaagcagagt      120
catggaaaaa gccttgagtg gattggagat attaatccct attctggtga aactacctac      180
aaccagaagt tcaagggcac ggccacatcg actgttagaca agtcttccag tatagcctac      240
atggagatcc gcggcctgac atctgaggac tctgcagtct attactgtgc aagagatgtat      300
tacgacgcct ctccgtttgc ttactggggc caagggactc tggtaactgt ctctgcagcc      360
aaaacgacac cccccatctgt ctatccactg gcccctggat ctgctgcca aactaactcc      420
atgggtgaccc tgggatgcct ggtcaaggcc tatttccctg agccagtgc acgtgacctgg      480
aactctggat ccctgtccag cggtgtgcac accttccag ctgtctgca gtctgaccc      540
tacactctga gcagctcagt gactgtcccc tccagcacct gcccagcga gaccgtcacc      600
tgcaacgttg cccacccggc cagcagcacc aaggtggaca agaaaattgt gcccaggat      660
tgtggttgt agccttgat atgtacagtc ccagaagttt catctgtctt catttcccc      720
ccaaagccca aggatgtgct caccattact ctgactccta aggtcacgtg tggtagatgt      780
gacatcagca aggatgtacc cgagggtccag ttcagctgg ttttagatgt tggaggtg      840
cacacagtc agacgcaacc cggggaggag cagttcaaca gcacttccg ctcagtcagt      900
gaacttccca tcatgcacca ggactggctc aatggcaagg agttcaaattt cagggtcaac      960
agtccagctt tccctgcccc catcgagaaa accatctcca aaaccaaaagg cagaccgaag      1020
gtcccacagg tgtacaccat tccacccccc aaggagcaga tggccaagga taaagtcaat      1080
ctgacctgca tgataacaga cttttccctt gaagacatta ctgtggagtg gcagtggat      1140
gggcagccag cggagaacta caagaacact cagccatca tggacacaga tggctttac      1200
ttcatctaca gcaagctcaa tgtgcagaag agcaactggg aggcaggaaa tactttcacc      1260
tgctctgtgt tacatgaggg cctgcacaac caccatactg agaagagcct ctccactct      1320
cctggtaat ga                                         1332

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<210> SEQ ID NO 13
<211> LENGTH: 462
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 13

Met Arg Cys Arg Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1 5 10 15

Val Leu Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Thr
20 25 30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asp His Tyr Met Ser Trp Val Lys Gln Ser His Gly Lys Ser Leu
50 55 60

Glu Trp Ile Gly Asp Ile Asn Pro Tyr Ser Gly Glu Thr Thr Tyr Asn

US 9,089,553 B2

39**40**

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| 65 | 70 | 75 | 80 |
|---|-----|-----|-----|
| Gln Lys Phe Lys Gly Thr Ala Thr Leu Thr Val Asp Lys Ser Ser Ser | | | |
| 85 | 90 | 95 | |
| Ile Ala Tyr Met Glu Ile Arg Gly Leu Thr Ser Glu Asp Ser Ala Val | | | |
| 100 | 105 | 110 | |
| Tyr Tyr Cys Ala Arg Asp Asp Tyr Asp Ala Ser Pro Phe Ala Tyr Trp | | | |
| 115 | 120 | 125 | |
| Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro | | | |
| 130 | 135 | 140 | |
| Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met | | | |
| 145 | 150 | 155 | 160 |
| Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr | | | |
| 165 | 170 | 175 | |
| Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro | | | |
| 180 | 185 | 190 | |
| Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val | | | |
| 195 | 200 | 205 | |
| Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His | | | |
| 210 | 215 | 220 | |
| Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys | | | |
| 225 | 230 | 235 | 240 |
| Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe | | | |
| 245 | 250 | 255 | |
| Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro | | | |
| 260 | 265 | 270 | |
| Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val | | | |
| 275 | 280 | 285 | |
| Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr | | | |
| 290 | 295 | 300 | |
| Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu | | | |
| 305 | 310 | 315 | 320 |
| Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys | | | |
| 325 | 330 | 335 | |
| Arg Val Asn Ser Pro Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser | | | |
| 340 | 345 | 350 | |
| Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro | | | |
| 355 | 360 | 365 | |
| Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile | | | |
| 370 | 375 | 380 | |
| Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly | | | |
| 385 | 390 | 395 | 400 |
| Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp | | | |
| 405 | 410 | 415 | |
| Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp | | | |
| 420 | 425 | 430 | |
| Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His | | | |
| 435 | 440 | 445 | |
| Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys | | | |
| 450 | 455 | 460 | |

<210> SEQ ID NO 14

<211> LENGTH: 1389

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

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<400> SEQUENCE: 14

| | |
|--|------|
| atgagatgca ggtggatctt tcttttctc ctgtcaggaa ctgcagggtgt cctctctgag | 60 |
| gtccagctgc aacagtctgg acctgaactg gtgacgcctg gggcttcagt gaagatatct | 120 |
| tgttaaggctt ctggatacac attcaactgac cactacatga gctgggtgaa gcagagtcata | 180 |
| ggaaaaagcc ttgagtggt tggagatatt aatccctatt ctggtgaaac tacctacaac | 240 |
| cagaagttca agggcgcgc cacattgact gtagacaagt cttccagttt acgcctacatg | 300 |
| gagatccgcg gcctgacatc tgaggactt gcaacttattt actgtgcaag agatgattac | 360 |
| gacgcctctc cgtttgccta ctggggccaa gggactctgg tcactgtctc tgccagccaaa | 420 |
| acgacaccccc catctgtcta tccactggcc cctggatctg ctgcccacaa taactccatg | 480 |
| gtgaccctgg gatgecttgtt caagggttat ttccctgaggc cagtgacagt gacctggAAC | 540 |
| tctggatccc tgcaccccg tgcacccacc ttccctgaggc tccctgaggc tgacccctac | 600 |
| actctgagca gtcagtgac tgcacccctcc agcacctggc ccagcgagac cgtcacctgc | 660 |
| aacgttgccc acccgcccg cagcaccaag gtggacaaga aaattgtgcc cagggattgt | 720 |
| ggtttgcataatg tacagtcataa gaagtatcat ctgtcttcat ctgcacccca | 780 |
| aagcccaagg atgtgtcac cattactctg actcctaagg tcacgtgtgt tgcgttagac | 840 |
| atcagcaagg atgatcccgaa ggtccagttc agctggttt tagatgtgtt ggagggtgcac | 900 |
| acagctcaga cgcaaccccg ggaggagcag ttcaacagca cttccgcctc agtcagtgaa | 960 |
| cttcccatca tgcaccagga ctggctcaat ggcaaggagt tcaaattgcag ggtcaacagt | 1020 |
| ccagcttcc ctgcacccat cgagaaaacc atctccaaaa ccaaaggcag accgaaggct | 1080 |
| ccacagggtgt acaccattcc acctccaaag gagcagatgg ccaaggataa agtcagtgaa | 1140 |
| acctgcatttca taacagactt cttccctgaa gacattactg tggagtggca gtggatggg | 1200 |
| cagccagccg agaactacaa gaacactcg cccatcatgg acacagatgg ctcttacttc | 1260 |
| atctacagca agtcataatgt gcagaagagc aactggagg cagaaatac tttcacctgc | 1320 |
| tctgtgttac atgagggcct gcacaaccac catactgaga agacgcctctc ccactctcct | 1380 |
| ggtaaatga | 1389 |

<210> SEQ ID NO 15

<211> LENGTH: 218

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 15

| | | | |
|---|---|----|----|
| Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Thr Val Ser Leu Gly | | | |
| 1 | 5 | 10 | 15 |

| | | |
|---|----|----|
| Leu Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp | | |
| 20 | 25 | 30 |

| | | |
|---|----|----|
| Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro | | |
| 35 | 40 | 45 |

| | | |
|---|----|----|
| Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala | | |
| 50 | 55 | 60 |

| | | | |
|---|----|----|----|
| Arg Phe Ser Gly Asn Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His | | | |
| 65 | 70 | 75 | 80 |

| | | |
|---|----|----|
| Pro Val Glu Glu Glu Asp Ala Val Thr Tyr Tyr Cys Gln Gln Ser Asn | | |
| 85 | 90 | 95 |

| | | |
|---|-----|-----|
| Glu Asp Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg | | |
| 100 | 105 | 110 |

-continued

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
 115 120 125
 Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
 130 135 140
 Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
 145 150 155 160
 Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
 165 170 175
 Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
 180 185 190
 His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
 195 200 205
 Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 210 215

<210> SEQ ID NO 16

<211> LENGTH: 657

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 16

```

gacattgtgc tgacccaatc tccagcttct ttgactgtgt ctctaggcct gagggccacc 60
atctcctgca aggccagcca aagtgtttag tatgtatggt atagttatata gaactggtag 120
cagcagaaac caggacagcc acccaaactc ctcatctatg ctgcataccaa tctagaatct 180
gggatcccag ccaggttttag tggcaatggg tctggacag acttcaccct caacatccat 240
cctgtggagg aggaggatgc tgtaacctat tactgtcaac aaagtaatga ggatccgtgg 300
acgttcgggtg gaggcacccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc 360
atcttccac catccagtga gcagttaca tctggaggtg cctcagtcgt gtgcttcttg 420
aacaacttct accccaaaga catcaatgtc aagtggaaaga ttgatggcag tgaacgacaa 480
aatggcgtcc tgaacagttg gactgatcg gacagcaaag acagcaccta cagcatgagc 540
agcacccctca cggtgacccaa ggacgagtagt gaacgacatac acagctatac ctgtgaggcc 600
actcacaaga catcaacttc acccattgtc aagagctca acaggaatga gtgttag 657

```

<210> SEQ ID NO 17

<211> LENGTH: 238

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 17

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Thr
 20 25 30

Val Ser Leu Gly Leu Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
 35 40 45

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
 50 55 60

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
 65 70 75 80

Gly Ile Pro Ala Arg Phe Ser Gly Asn Gly Ser Gly Thr Asp Phe Thr
 85 90 95

Leu Asn Ile His Pro Val Glu Glu Asp Ala Val Thr Tyr Tyr Cys

-continued

| | | | |
|---|-----|-------------|-----|
| 100 | 105 | 110 | |
| Gln Gln Ser Asn Glu Asp Pro Trp Thr Phe Gly Gly Gly | | Thr Lys Leu | |
| 115 | 120 | 125 | |
| Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro | | | |
| 130 | 135 | 140 | |
| Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu | | | |
| 145 | 150 | 155 | 160 |
| Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly | | | |
| 165 | 170 | 175 | |
| Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser | | | |
| 180 | 185 | 190 | |
| Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp | | | |
| 195 | 200 | 205 | |
| Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr | | | |
| 210 | 215 | 220 | |
| Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys | | | |
| 225 | 230 | 235 | |

<210> SEQ ID NO 18

<211> LENGTH: 717

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 18

| | |
|--|-----|
| atggagacag acacaatcct gctatgggtg ctgctgctct gggttccagg ctccactgg | 60 |
| gacattgtgc tgacccaatc tccagcttct ttgactgtgt ctctaggcct gagggccacc | 120 |
| atctcctgca aggccagcca aagtgttgat tatgtatggg atagttatat gaactggtag | 180 |
| cagcagaaac caggacagcc acccaaactc ctcatctatg ctgcatccaa tctagaatct | 240 |
| gggatcccag ccaggttag tggcaatggg tctggacag acttcaccct caacatccat | 300 |
| cctgtggagg aggaggatgc tgtaacctat tactgtcaac aaagtaatga ggatccgtgg | 360 |
| acgttcggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc | 420 |
| atcttccac catccagtga gcagttaca tctggaggtg ctcagtcgt gtgcttctg | 480 |
| aacaacttct accccaaaga catcaatgtc aagtggaaata ttgatggcag tgaacgacaa | 540 |
| aatggcgctcc tgaacagttg gactgatcgac gacagcaag acagcaccta cagcatgagc | 600 |
| agcaccctca cggtgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc | 660 |
| actcacaaga catcaacttc acccattgtc aagagcttca acaggaatga gtgttag | 717 |

<210> SEQ ID NO 19

<211> LENGTH: 449

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 19

| | | | |
|---|----|----|----|
| Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Thr | | | |
| 1 | 5 | 10 | 15 |
| Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Cys | | | |
| 20 | 25 | 30 | |
| Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile | | | |
| 35 | 40 | 45 | |
| Gly Asp Ile Asn Pro Phe Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe | | | |
| 50 | 55 | 60 | |
| Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr | | | |

US 9,089,553 B2

47

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48

| 65 | 70 | 75 | 80 |
|-------------------------|-------------------------|---------------------|-------------|
| Met Gln Leu Asn Ser | Leu Thr Ser Asp Asp | Ser Ala Val Tyr | Tyr Cys |
| 85 | 90 | 95 | |
| Ala Arg Ser His | Tyr Tyr Phe Asp Gly | Arg Val Pro Trp | Asp Ala Met |
| 100 | 105 | 110 | |
| Asp Tyr Trp Gly Gln | Gly Thr Ser Val Thr Val | Ser Ala Lys | Thr |
| 115 | 120 | 125 | |
| Thr Pro Pro Ser Val | Tyr Pro Leu Ala Pro Gly | Ser Ala Ala Gln | Thr |
| 130 | 135 | 140 | |
| Asn Ser Met Val Thr | Leu Gly Cys Leu Val | Lys Gly Tyr Phe Pro | Glu |
| 145 | 150 | 155 | 160 |
| Pro Val Thr Val Thr | Trp Asn Ser Gly Ser | Leu Ser Ser Gly | Val His |
| 165 | 170 | 175 | |
| Thr Phe Pro Ala Val | Leu Gln Ser Asp | Leu Tyr Thr Leu Ser | Ser Ser |
| 180 | 185 | 190 | |
| Val Thr Val Pro Ser | Ser Thr Trp Pro Ser | Glu Thr Val Thr | Cys Asn |
| 195 | 200 | 205 | |
| Val Ala His Pro Ala Ser | Ser Thr Lys Val Asp | Lys Lys Ile Val Pro | |
| 210 | 215 | 220 | |
| Arg Asp Cys Gly Cys | Lys Pro Cys Ile Cys | Thr Val Pro Glu | Val Ser |
| 225 | 230 | 235 | 240 |
| Ser Val Phe Ile Phe | Pro Pro Lys Pro | Lys Asp Val | Leu Thr |
| 245 | 250 | 255 | |
| Leu Thr Pro Lys Val | Thr Cys Val Val Asp | Ile Ser Lys Asp | Asp |
| 260 | 265 | 270 | |
| Pro Glu Val Gln Phe | Ser Trp Phe Val Asp | Asp Val Glu | Val His Thr |
| 275 | 280 | 285 | |
| Ala Gln Thr Gln Pro | Arg Glu Gln Phe Asn | Ser Thr Phe Arg | Ser |
| 290 | 295 | 300 | |
| Val Ser Glu Leu Pro | Ile Met His Gln Asp | Trp Leu Asn Gly | Lys Glu |
| 305 | 310 | 315 | 320 |
| Phe Lys Cys Arg Val | Asn Ser Ala Ala Phe | Pro Ala Pro Ile Glu | Lys |
| 325 | 330 | 335 | |
| Thr Ile Ser Lys Thr | Lys Gly Arg Pro | Lys Ala Pro Gln | Val Tyr Thr |
| 340 | 345 | 350 | |
| Ile Pro Pro Pro Lys | Glu Gln Met Ala Lys Asp | Lys Val Ser | Leu Thr |
| 355 | 360 | 365 | |
| Cys Met Ile Thr Asp | Phe Phe Pro Glu Asp | Ile Thr Val Glu | Trp Gln |
| 370 | 375 | 380 | |
| Trp Asn Gly Gln Pro | Ala Glu Asn Tyr | Lys Asn Thr Gln | Pro Ile Met |
| 385 | 390 | 395 | 400 |
| Asp Thr Asp Gly Ser | Tyr Phe Ile Tyr | Ser Lys Leu Asn | Val Gln Lys |
| 405 | 410 | 415 | |
| Ser Asn Trp Glu Ala | Gly Asn Thr Phe | Thr Cys Ser Val | Leu His Glu |
| 420 | 425 | 430 | |
| Gly Leu His Asn His | His Thr Glu Lys | Ser Leu Ser His | Ser Pro Gly |
| 435 | 440 | 445 | |
| Lys | | | |

<210> SEQ_ID NO 20
<211> LENGTH: 1350
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

US 9,089,553 B2

49**50**

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<400> SEQUENCE: 20

| | |
|--|------|
| gagggtccagc tgcaacaatc tggacctgag ctgggtgaagc ctggggacttc agtgaagatg | 60 |
| tccctgttaagg cttctggata cacattcaact gactgctaca tgaactgggt gaagcagagc | 120 |
| catggaaaga gccttgaatg gattggagat attaattctt tcaacgggtgg tactacctac | 180 |
| aaccagaagt tcaagggcaa ggccacattt actgttagaca aatccctccag cacagctac | 240 |
| atgcagctca acagectgac atctgacgac tctgcagtct attactgtgc aagatcccat | 300 |
| tattacttcg atggtagagt cccttggat gctatggact actggggtca aggaacctca | 360 |
| gtcacccgtct cctcagccaa aacgacaccc ccatctgtct atccactggc ccctggatct | 420 |
| gtgtgcccaaa ctaactccat ggtgaccctg ggatgcctgg tcaagggcta ttccctgag | 480 |
| ccagtgacag tgacctggaa ctctggatcc ctgtccagcg gtgtgcacac ctccccagct | 540 |
| gtcctgcagt ctgacccctta cactctgago agtcagtga ctgtcccttc cagcacctgg | 600 |
| cccagcgaga ccgtcacctg caacgttgcc caccggcca gcagcaccaa ggtggacaag | 660 |
| aaaatttgtc ccagggattt tggttgtaa ccttgcataat gtacagtccc agaagtatca | 720 |
| tctgtttca tcttccccc aaagcccaag gatgtgtca ccattactct gactcctaag | 780 |
| gtcacgtgtg ttgtggtaga catcagcaag gatgatecccg aggtccagtt cagctggttt | 840 |
| gttagatgtatg tggaggtgca cacagcttag acgcaacccc gggaggagca gttcaacagc | 900 |
| actttccgct cagtcagtga acttccatc atgcaccagg actggctcaa tggcaaggag | 960 |
| ttcaaatgca gggtaaacag tgcagcttc cctgccccca tcgagaaaaac catctccaaa | 1020 |
| accaaaggca gaccgaaggc tccacagggt tacaccattc cacccctccaa ggagcagatg | 1080 |
| gcccaaggata aagtcagtct gacctgcatg ataacagact tcttccctga agacattact | 1140 |
| gtggagtgcc agtggaaatgg gcagccagcg gagaactaca agaacactca gcccattatg | 1200 |
| gacacagatg gctttactt catctacago aagctcaatg tgcagaagag caactggag | 1260 |
| gcaggaaata ctttcacctg ctctgtgtta catgagggcc tgcacaacca ccatactgag | 1320 |
| aagagcctct cccactctcc tggtaatga | 1350 |

<210> SEQ ID NO 21

<211> LENGTH: 468

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 21

| | |
|---|--|
| Met Gly Trp Asn Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly | |
| 1 5 10 15 | |
| Val Tyr Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys | |
| 20 25 30 | |
| Pro Gly Thr Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe | |
| 35 40 45 | |
| Thr Asp Cys Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu | |
| 50 55 60 | |
| Glu Trp Ile Gly Asp Ile Asn Pro Phe Asn Gly Gly Thr Thr Tyr Asn | |
| 65 70 75 80 | |
| Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser | |
| 85 90 95 | |
| Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Asp Asp Ser Ala Val | |
| 100 105 110 | |
| Tyr Tyr Cys Ala Arg Ser His Tyr Tyr Phe Asp Gly Arg Val Pro Trp | |
| 115 120 125 | |

-continued

Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 130 135 140
 Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
 145 150 155 160
 Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
 165 170 175
 Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
 180 185 190
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
 195 200 205
 Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
 210 215 220
 Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
 225 230 235 240
 Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro
 245 250 255
 Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
 260 265 270
 Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser
 275 280 285
 Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu
 290 295 300
 Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr
 305 310 315 320
 Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn
 325 330 335
 Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro
 340 345 350
 Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln
 355 360 365
 Val Tyr Thr Ile Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val
 370 375 380
 Ser Leu Thr Cys Met Ile Thr Asp Phe Pro Glu Asp Ile Thr Val
 385 390 395 400
 Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln
 405 410 415
 Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn
 420 425 430
 Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val
 435 440 445
 Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
 450 455 460
 Ser Pro Gly Lys
 465

<210> SEQ ID NO 22
 <211> LENGTH: 1407
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 22

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| atgggatgga | actggatctt | tctttcctc | ttgtcaggaa | ctgcagggtgt | ctactctgag | 60 |
| gtccagctgc | aacaatctgg | acctgagctg | gtgaagcctg | ggacttcagt | gaagatgtcc | 120 |

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| | | | | | | |
|--------------|-------------|-------------|------------|-------------|------------|------|
| tgttaaggcctt | ctggatacac | attcaactgac | tgctacatga | actgggtgaa | gcagagccat | 180 |
| gggaagagcc | ttgaatggat | tggagatatt | aatccttca | acgggtggac | tacctacaac | 240 |
| cagaagttca | aggccaaggc | cacattgact | gtagacaaat | cctccagcac | agcctacatg | 300 |
| cagctcaaca | gcctgacatc | tgacgactct | gcagtttat | actgtgcaag | atcccattat | 360 |
| tacttcgatg | gttagagtccc | ttgggatgtct | atggactact | ggggtaaagg | aacctcagtc | 420 |
| accgtctcc | cagccaaaac | gacaccccca | tctgtctatc | cactggcccc | tggatctgct | 480 |
| gcccaaacta | actccatggt | gaccctggga | tgcttgtca | agggctattt | ccctgaggca | 540 |
| gtgacagtga | cctggaactc | tggatccctg | tccagcggtg | tgcacacctt | cccgactgtc | 600 |
| ctgcagtctg | acctctacac | tctgagcagc | tcagtgaatg | tccctccag | cacctggccc | 660 |
| agcgagaccc | tcacctgcaa | cgtgcccac | ccggccagca | gcaccaaggt | ggacaagaaa | 720 |
| atttgtccca | gggattgtgg | ttgttaagct | tgcatatgt | cagtcccaga | agtatcatct | 780 |
| gtcttcatct | tccccccaaa | gccccaggat | gtgctcacca | ttactctgac | tcctaaggc | 840 |
| acgtgtgttg | ttgttagacat | cagcaaggat | gatcccagg | tccagttcag | ctggttgt | 900 |
| gtatgtgtgg | aggtgcacac | agctcagacg | caaccccggg | aggagcagtt | caacagcact | 960 |
| ttccgctcag | tcagtgaact | tcccatcatg | caccaggact | ggctcaatgg | caaggagttc | 1020 |
| aaatgcaggg | tcaacagtgc | agctttccct | gccccatcg | agaaaaaccat | ctccaaaacc | 1080 |
| aaaggcagac | cgaaggctcc | acagggtgtac | accattccac | ctcccaagga | gcagatggcc | 1140 |
| aaggataaaag | tcagtctgac | ctgcatgata | acagacttct | tccctgaaga | cattactgt | 1200 |
| gagttggcagt | ggaatggca | gccagcggag | aactacaaga | acactcagcc | catcatggac | 1260 |
| acagatggct | cttacttcat | ctacagcaag | ctcaatgtc | agaagagcaa | ctggaggca | 1320 |
| ggaaataactt | tcacctgctc | tgtgttacat | gagggcctgc | acaaccacca | tactgagaag | 1380 |
| agectctccc | actctcctgg | taaatga | | | | 1407 |

<210> SEQ_ID NO 23

<211> LENGTH: 217

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: Rabbit-mouse chimera

<400> SEQUENCE: 23

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Val | Leu | Thr | Gln | Thr | Pro | Ala | Ser | Val | Ser | Ala | Ala | Val | Gly |
| 1 | | | | | | | | 10 | | | | 15 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Thr | Val | Thr | Ile | Asn | Cys | Gln | Ser | Ser | Gln | Ser | Val | Tyr | Asp | Asn |
| | | | | 20 | | | | 25 | | | | 30 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Trp | Leu | Ala | Trp | Phe | Gln | Gln | Lys | Pro | Gly | Gln | Pro | Pro | Lys | Leu |
| | | | | | 35 | | | 40 | | | 45 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Tyr | Asp | Ala | Ser | Asp | Leu | Ala | Ser | Gly | Val | Pro | Ser | Arg | Phe |
| | | | | | 50 | | | 55 | | | 60 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Gly | Ser | Gly | Thr | Gln | Phe | Thr | Leu | Thr | Ile | Ser | Gly | Val |
| | | | | | 65 | | | 70 | | | 75 | | | 80 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Cys | Ala | Asp | Ala | Ala | Thr | Tyr | Tyr | Cys | Gln | Gly | Ala | Tyr | Asn | Asp |
| | | | | | | 85 | | | 90 | | | 95 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Ile | Tyr | Ala | Phe | Gly | Gly | Thr | Glu | Val | Val | Val | Lys | Arg | Thr | |
| | | | | | 100 | | | 105 | | | | 110 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ala | Ala | Pro | Thr | Val | Ser | Ile | Phe | Pro | Pro | Ser | Ser | Glu | Gln | Leu |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

US 9,089,553 B2

55**56**

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115 120 125

Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro
 130 135 140

Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn
 145 150 155 160

Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr
 165 170 175

Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His
 180 185 190

Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile
 195 200 205

Val Lys Ser Phe Asn Arg Asn Glu Cys
 210 215

<210> SEQ ID NO 24

<211> LENGTH: 654

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polynucleotide

<220> FEATURE:

<221> NAME/KEY: misc_feature

<223> OTHER INFORMATION: Rabbit-mouse chimera

<400> SEQUENCE: 24

```

gcgcaagtgc tgacccagac tccagcctcc gtgtctgcag ctgtggagg cacagtacc 60
atcaattgcc agtccagtca gagtgtttat gataacaact ggtagcctg gttcagcag 120
aaaccagggc agcctcccaa gctcctgatt tatgatgcat ccgatctggc atctgggtc 180
ccatcgcggt tcagtgccag tggatctggg acacagttca ctctcaccat cagcggcgtg 240
cagtgcccg atgctgccac ttactactgt caaggcgctt ataatgatgt tatttatgct 300
ttcggggag ggacccgggt ggtggtaaa cgtacggatg ctgcaccaac tgtatccatc 360
ttccccaccat ccagtggca gttAACATCT ggaggtgcct cagtcgtgtg cttctgaac 420
aacttctacc ccaaagacat caatgtcaag tggaaagattt atggcagtga acgacaaaat 480
ggcgctctga acagttggac tgatcaggac agcaaagaca gcacccatcag catgagcagc 540
accctcacgt tgaccaagga cgagttatgaa cgacataaca gctataccctg tgaggccact 600
cacaagacat caacttcacc cattgtcaag agcttcaaca ggaatgagtg ttag 654

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<210> SEQ ID NO 25

<211> LENGTH: 239

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: Rabbit-mouse chimera

<400> SEQUENCE: 25

Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15

Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Thr Pro Ala Ser
 20 25 30

Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser Ser
 35 40 45

Gln Ser Val Tyr Asp Asn Asn Trp Leu Ala Trp Phe Gln Gln Lys Pro
 50 55 60

-continued

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asp Leu Ala Ser
65 70 75 80

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Thr
85 90 95

Leu Thr Ile Ser Gly Val Gln Cys Ala Asp Ala Ala Thr Tyr Tyr Cys
100 105 110

Gln Gly Ala Tyr Asn Asp Val Ile Tyr Ala Phe Gly Gly Thr Glu
115 120 125

Val Val Val Lys Arg Thr Asp Ala Ala Pro Thr Val Ser Ile Phe Pro
130 135 140

Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe
145 150 155 160

Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp
165 170 175

Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp
180 185 190

Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys
195 200 205

Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys
210 215 220

Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225 230 235

<210> SEQ ID NO 26
<211> LENGTH: 720
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic nucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Rabbit-mouse chimera

<400> SEQUENCE: 26

atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60
acatttgcgc aagtgttgac ccagactcca gcctccgtgt ctgcagctgt gggaggcaca 120
gtcaccatca attgecagtc cagtcagagt gtttatgata acaactgggtt agcctggttt 180
cagcagaaac cagggcagcc tcccaagtc ctgattttagt atgcattccga tctggcatct 240
ggggtccccat cgcggttcag tggcgttgaa tctgggacac agttcactct caccatcagc 300
ggcgtgcagt gtgccatgc tgccacttac tactgtcaag gcgcttataa tggatgttatt 360
tatgcttcg gcggagggac cgagggtggtg gtcaaacgtt cggatgtgc accaactgtta 420
tccatcttcc caccatccag tgagcgtt acatctggag gtgcctcagt cgtgtgtttc 480
ttgaacaact tctacccaa agacatcaat gtcaagtggaa agattgtatgg cagtgtacga 540
caaaatggcg ttctgaacag ttggactgtt caggacacaa aagacacac ctacacatgt 600
agcagcaccc tcacgttgac caaggacgag tatgaacgac ataacagcta tacctgttag 660
gcacactcaca agacatcaac ttcacccatt gtcaagagctt tcaacaggaa tgagtgttag 720

<210> SEQ ID NO 27
<211> LENGTH: 433
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:

US 9,089,553 B2

59**60**

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<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: Humanized Antibody

<400> SEQUENCE: 27

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ser | Leu | Glu | Glu | Ser | Gly | Gly | Arg | Leu | Val | Thr | Pro | Gly | Thr | Pro |
| 1 | | | | | | | | | | | | | | | |
| | | | | | | | | | 5 | 10 | | | 15 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Thr | Leu | Thr | Cys | Thr | Ala | Ser | Gly | Phe | Ser | Leu | Ser | Ser | Tyr | Trp |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 20 | 25 | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Trp | Val | Arg | Gln | Ala | Pro | Gly | Glu | Gly | Leu | Glu | Trp | Ile | Gly |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 35 | 40 | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Asp | Ser | Gly | Gly | Arg | Thr | Asp | Tyr | Ala | Ser | Trp | Ala | Lys | Gly |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 50 | 55 | | 60 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Phe | Thr | Ile | Ser | Arg | Thr | Ser | Thr | Thr | Met | Asp | Leu | Lys | Met | Thr |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 65 | 70 | | 75 | | 80 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Thr | Thr | Gly | Asp | Thr | Ala | Arg | Tyr | Phe | Cys | Ala | Arg | Asn | Trp |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 85 | 90 | | 95 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Trp | Gly | Gln | Gly | Thr | Leu | Val | Thr | Val | Ser | Ser | Ala | Ser | Thr |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 100 | 105 | | 110 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gly | Pro | Ser | Val | Tyr | Pro | Leu | Ala | Pro | Gly | Ser | Ala | Ala | Gln | Thr |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 115 | 120 | | 125 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Met | Val | Thr | Leu | Gly | Cys | Leu | Val | Lys | Gly | Tyr | Phe | Pro | Glu |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 130 | 135 | | 140 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Val | Thr | Val | Thr | Trp | Asn | Ser | Gly | Ser | Leu | Ser | Ser | Gly | Val | His |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 145 | 150 | | 155 | | 160 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser | Asp | Leu | Tyr | Thr | Leu | Ser | Ser | Ser |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 165 | 170 | | 175 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Val | Pro | Ser | Ser | Thr | Trp | Pro | Ser | Glu | Thr | Val | Thr | Cys | Asn |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 180 | 185 | | 190 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | His | Pro | Ala | Ser | Ser | Thr | Lys | Val | Asp | Lys | Lys | Ile | Val | Pro |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 195 | 200 | | 205 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Asp | Cys | Gly | Cys | Lys | Pro | Cys | Ile | Cys | Thr | Val | Pro | Glu | Val | Ser |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 210 | 215 | | 220 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Phe | Ile | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Val | Leu | Thr | Ile | Thr |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 225 | 230 | | 235 | | 240 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Thr | Pro | Lys | Val | Thr | Cys | Val | Val | Val | Asp | Ile | Ser | Lys | Asp | Asp |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 245 | 250 | | 255 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Glu | Val | Gln | Phe | Ser | Trp | Phe | Val | Asp | Asp | Val | Glu | Val | His | Thr |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 260 | 265 | | 270 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Thr | Gln | Pro | Arg | Glu | Glu | Gln | Phe | Asn | Ser | Thr | Phe | Arg | Ser |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 275 | 280 | | 285 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Glu | Leu | Pro | Ile | Met | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys | Glu |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 290 | 295 | | 300 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Lys | Cys | Arg | Val | Asn | Ser | Ala | Ala | Phe | Pro | Ala | Pro | Ile | Glu | Lys |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 305 | 310 | | 315 | | 320 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Ser | Lys | Thr | Lys | Gly | Arg | Pro | Lys | Ala | Pro | Gln | Val | Tyr | Thr |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 325 | 330 | | 335 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Pro | Pro | Lys | Glu | Gln | Met | Ala | Lys | Asp | Lys | Val | Ser | Leu | Thr | |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 340 | 345 | | 350 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Met | Ile | Thr | Asp | Phe | Phe | Pro | Glu | Asp | Ile | Thr | Val | Glu | Trp | Gln |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 355 | 360 | | 365 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Asn | Gly | Gln | Pro | Ala | Glu | Asn | Tyr | Lys | Asn | Thr | Gln | Pro | Ile | Met |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 370 | 375 | | 380 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Thr | Asn | Gly | Ser | Tyr | Phe | Val | Tyr | Ser | Lys | Leu | Asn | Val | Gln | Lys |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | 385 | 390 | | 395 | | 400 | |

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Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu
405 410 415

Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
 420 425 430

Lys

```
<210> SEQ ID NO 29
<211> LENGTH: 452
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody
```

<400> SEQUENCE: 29

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Met Glu Thr Gly Leu Arg Trp Leu Leu Val Ala Val Leu Lys Gly
 1 5 10 15

Val His Cys Gln Ser Leu Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
 20 25 30

Gly Thr Pro Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Leu Ser
 35 40 45

Ser Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Glu
 50 55 60

Trp Ile Gly Thr Ile Asp Ser Gly Gly Arg Thr Asp Tyr Ala Ser Trp
 65 70 75 80

Ala Lys Gly Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Met Asp Leu
 85 90 95

Lys Met Thr Ser Leu Thr Thr Gly Asp Thr Ala Arg Tyr Phe Cys Ala
 100 105 110

Arg Asn Trp Asn Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

Ala Ser Thr Lys Gly Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
 130 135 140

Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
 145 150 155 160

Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
 165 170 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
 180 185 190

Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
 195 200 205

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
 210 215 220

Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro
 225 230 235 240

Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
 245 250 255

Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser
 260 265 270

Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu
 275 280 285

Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr
 290 295 300

Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn
 305 310 315 320

Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro
 325 330 335

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln
 340 345 350

Val Tyr Thr Ile Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val
 355 360 365

Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val
 370 375 380

Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln
 385 390 395 400

Pro Ile Met Asn Thr Asn Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn
 405 410 415

Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val

-continued

Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
435 440 445

Ser Pro Gly Lys
450

```
<210> SEQ ID NO 30
<211> LENGTH: 1359
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody
```

<400> SEQUENCE: 30

| | |
|---|------|
| atggagactg ggctcgctg gctctcccg tgcgtgtgc tcaaaggtgt ccactgtcag | 60 |
| tcgctggagg agtccggggg tcgcctggtc acgcctggaa caccctgac actcacctgc | 120 |
| acagcctctg gatttccct cagtagttat tggatgaact gggtcggcca ggctccaggg | 180 |
| gaggggtctgg aatggatcg aaccattgtat tctgggtgta ggacggacta cgcgagctgg | 240 |
| gcaaaaaggcc gattcccat ctccagaacc tcgactacgaa tggatctgaa aatgaccagt | 300 |
| ctgacgaccc gggacacggc ccgttatttc tggccagaaa attgaaacctt gtggggccaa | 360 |
| ggcacccctcg tcaccgtctc gagcgcttct acaaaggccc catctgtcta tccactggcc | 420 |
| cctggatctg ctgccccaaac taactccatg gtgaccctgg gatgcctggt caaggctat | 480 |
| tccctgagc cagtgcacgt gacctggAAC tctggatccc tggccagcgg tgcacacc | 540 |
| tccctcagctg tcctgcagtc tgacctctac actctgagca gtcagtgac tggccctcc | 600 |
| agcacctggc ccagcgagac cgtcacctgc aacgttgcac acccggccag cagcaccaag | 660 |
| gtggacaaga aaattgtgcc cagggattgt ggttgaagc cttgcataatg tacagtccca | 720 |
| gaagtatcat ctgtcttcat cttccccca aagcccaagg atgtgctcac cattactctg | 780 |
| actcctaagg tcacgtgtgt tgggttagac atcagaagg atgatcccga ggtccagttc | 840 |
| agctgggttg tagatgtatgg gggatgtcac acagctaga cgcaaccccg ggaggagcag | 900 |
| ttcaacagca cttccgctc agtcagtgaa cttccatca tgcaccagga ctggctcaat | 960 |
| ggcaaggagt tcaaatacgat ggtcaacagt gcagcttcc ctggcccccattt cgaaaaacc | 1020 |
| atctccaaaa ccaaaggccag accgaaggctt ccacagggtt acaccattcc acctcccaag | 1080 |
| gagcagatgg ccaaggataa agtcagtgatgg acctgcataa taacagactt cttccctgaa | 1140 |
| gacattactg tggagtggca gtggaatggg cagccagcgg agaactacaa gaacactcag | 1200 |
| cccatcatgg acacagatgg ctcttacttc gtctacagca agctcaatgt gcagaagacg | 1260 |
| aactggggggg cagggaaatac tttcacctgc tctgtgttac atgagggcct gcacaaccac | 1320 |
| catactgaga agagcctctc ccactctctt ggtaaatga | 1359 |

<210> SEQ ID NO 31
<211> LENGTH: 213
<212> TYPE: PRT
<213> ORGANISM: *Mus musculus*

<400> SEQUENCE: 31

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ile | Val | Leu | Thr | Gln | Ser | Pro | Thr | Ile | Val | Ser | Ala | Ser | Pro | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

Glu Lys Val Thr Leu Ile Cys Ser Ala Ser Ser Ser Val Ser Phe Val

US 9,089,553 B2

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20 25 30

Asp Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp Ile Tyr
 35 40 45

Arg Thr Ser Asn Leu Gly Phe Gly Val Pro Ala Arg Phe Ser Gly Gly
 50 55 60

Gly Ser Gly Thr Ser His Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Thr Tyr Pro Pro Thr
 85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala Pro
 100 105 110

Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly
 115 120 125

Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn
 130 135 140

Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn
 145 150 155 160

Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
 165 170 175

Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr
 180 185 190

Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe
 195 200 205

Asn Arg Asn Glu Cys
 210

<210> SEQ ID NO 32

<211> LENGTH: 642

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 32

```

caaaattgttc tcacccagtc tccaacaatc gtgtctgcat ctccaggggga gaaggtcacc 60
ctaatctgca gtgcccgatc aagtgttaatg ttctgtggact ggttccagca gaagccaggc 120
acttctccca aacgctggat ttacagaaca tccaacctgg gttttggagt ccctgctcgc 180
ttcagtgccg gtggatctgg gacctctcac tctctcacaa tcagccgaat ggaggctgaa 240
gatgctgcca cttattactg ccagcaaagg agtacttacc caccacgtt cggtgctgg 300
accaagctgg aactgaaacg ggctgtatgt gcaccaactg tatccatctt cccaccatcc 360
agtgagcagt taacatctgg aggtgcctca gtcgtgtgct tcttgaacaa cttctacccc 420
aaagacatca atgtcaagtg gaagattgat ggcagtgaac gacaaaatgg cgtcctgaac 480
agttggactg atcaggacag caaagacagc acctacagca tgagcagcac cctcacgttg 540
accaaggacg agtatgaacg acataacagc tataacctgtg aggccactca caagacatca 600
acttcaccca ttgtcaagag cttcaacagg aatgagtgtt ag 642

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<210> SEQ ID NO 33

<211> LENGTH: 235

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 33

Met His Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Val | Ser | Arg | Gly | Gln | Ile | Val | Leu | Thr | Gln | Ser | Pro | Thr | Ile |
| 20 | | | | | | | 25 | | | | | | 30 | | |
| Val | Ser | Ala | Ser | Pro | Gly | Glu | Lys | Val | Thr | Leu | Ile | Cys | Ser | Ala | Ser |
| 35 | | | | | | | 40 | | | | | 45 | | | |
| Ser | Ser | Val | Ser | Phe | Val | Asp | Trp | Phe | Gln | Gln | Lys | Pro | Gly | Thr | Ser |
| 50 | | | | | | | 55 | | | | | 60 | | | |
| Pro | Lys | Arg | Trp | Ile | Tyr | Arg | Thr | Ser | Asn | Leu | Gly | Phe | Gly | Val | Pro |
| 65 | | | | | | | 70 | | | | 75 | | | | 80 |
| Ala | Arg | Phe | Ser | Gly | Gly | Gly | Ser | Gly | Thr | Ser | His | Ser | Leu | Thr | Ile |
| 85 | | | | | | | 90 | | | | | | 95 | | |
| Ser | Arg | Met | Glu | Ala | Glu | Asp | Ala | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Arg |
| 100 | | | | | | | 105 | | | | | | 110 | | |
| Ser | Thr | Tyr | Pro | Pro | Thr | Phe | Gly | Ala | Gly | Thr | Lys | Leu | Glu | Leu | Lys |
| 115 | | | | | | | 120 | | | | | | 125 | | |
| Arg | Ala | Asp | Ala | Ala | Pro | Thr | Val | Ser | Ile | Phe | Pro | Pro | Ser | Ser | Glu |
| 130 | | | | | | | 135 | | | | | | 140 | | |
| Gln | Leu | Thr | Ser | Gly | Gly | Ala | Ser | Val | Val | Cys | Phe | Leu | Asn | Asn | Phe |
| 145 | | | | | | | 150 | | | | | 155 | | | 160 |
| Tyr | Pro | Lys | Asp | Ile | Asn | Val | Lys | Trp | Lys | Ile | Asp | Gly | Ser | Glu | Arg |
| 165 | | | | | | | | | 170 | | | | | 175 | |
| Gln | Asn | Gly | Val | Leu | Asn | Ser | Trp | Thr | Asp | Gln | Asp | Ser | Lys | Asp | Ser |
| 180 | | | | | | | | 185 | | | | | 190 | | |
| Thr | Tyr | Ser | Met | Ser | Ser | Thr | Leu | Thr | Leu | Thr | Lys | Asp | Glu | Tyr | Glu |
| 195 | | | | | | | 200 | | | | | | 205 | | |
| Arg | His | Asn | Ser | Tyr | Thr | Cys | Glu | Ala | Thr | His | Lys | Thr | Ser | Thr | Ser |
| 210 | | | | | | | 215 | | | | | 220 | | | |
| Pro | Ile | Val | Lys | Ser | Phe | Asn | Arg | Asn | Glu | Cys | | | | | |
| 225 | | | | | | | 230 | | | | | 235 | | | |

<210> SEQ ID NO 34
<211> LENGTH: 708
<212> TYPE: DNA
<213> ORGANISM: *Mus musculus*

<400> SEQUENCE: 34

atgcatttc aagtgcagat ttccagcttc ctgtcaatac gtgcctcagg catagtgcc
agaggcaaa ttgttctcac ccagtctcca acaatcggtt ctgcacatcc aggggagaag 120
gtcacccata tctcgagtc cagttcaagt gtaagtttc tggaactgggtt ccagcagaag
ccaggcactt ctcccaaacg ctggatttac agaacatcca acctgggtt tggagtcct 240
gttcgttca gtggcggtgg atctgggacc tctcactctc tcacaatcag ccgaatggag
gctgaagatg ctgcccactta ttactgcacaaaggactt cttaccacc cacgttcgg 360
gctgggacca agcttggaaact gaaacgggtt gatgctgcac caactgtatc catttccca
ccatccagtg agcagttaac atctggaggt gcctcagttcg tttgtttttt gaacaacttc
taccccaaag acatcaatgt caagtggaaat ttgatggca gtgaacgcaca aaatggcg 540
ctgaacagggtt ggactgtatca ggacacgcaaa gagacgcacat acagcatgag cagccaccc
acgttgacca aggacgagta tgaacgcacat aacagctata cctgtgaggc cactcacaag 660
acatcaacctt caccattttt caaqaqcttc aacaqqaaatq aqtqttqaq 708

<210> SEQ ID NO 35

<211> LENGTH: 449

<212> TYPE: PRT

<212> TYPE: PRT
<213> ORGANISM: *Mus musculus*

-continued

<400> SEQUENCE: 35

Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Met Gly Val Gly Trp Ile Arg His Pro Ser Gly Lys Asn Leu Glu
35 40 45

Trp Leu Ala His Ile Trp Trp Asp Asp Val Lys Arg Tyr Asn Pro Val
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Asn Ser Gln Val
65 70 75 80

Phe Leu Lys Ile Ala Asn Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Glu Asp Phe Asp Tyr Asp Glu Glu Tyr Tyr Ala Met
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Ser Val Ile Val Ser Ser Ala Lys Thr
115 120 125

Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr
130 135 140

Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu
145 150 155 160

Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
180 185 190

Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
195 200 205

Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
210 215 220

Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser
225 230 235 240

Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr
245 250 255

Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp
260 265 270

Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr
275 280 285

Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser
290 295 300

Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr
340 345 350

Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr
355 360 365

Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
370 375 380

Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
385 390 395 400

Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys

-continued

| | | |
|-----|-----|-----|
| 405 | 410 | 415 |
|-----|-----|-----|

Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu
420 425 430

Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
435 440 445

Lys

<210> SEQ ID NO 36

<211> LENGTH: 1350

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 36

| | |
|---|------|
| caggttactc tgaaagagtc tggccctggg atattgcagc cctcccagac cctcagtgctg | 60 |
| acttgttctt tctctgggtt ttcaactgagc acttctggta tgggtgttagg ctggattcgt | 120 |
| cacccatcg ggaagaatct ggagtggctg gcacacattt ggtggatga tgtcaagcgc | 180 |
| tataaccagg tcctgaagag ccgactgact atctccaagg atacctccaa cagccaggt | 240 |
| ttcctcaaga tcgccaatgt ggacactgca gatactgccata tactactg tgctcgaata | 300 |
| gaggactttg attacgacga ggagtattat gctatggact actggggtca aggaacctca | 360 |
| gtcatcgct cctcagccaa aacgacaccc ccatctgtct atccactggc ccctggatct | 420 |
| gctgccccaa ctaactccat ggtgaccctg ggatgcctgg tcaaggccta tttccctgag | 480 |
| ccagtgcacag tgacctggaa ctctggatcc ctgtccagcg gtgtgcacac cttccagct | 540 |
| gtcctgcagt ctgaccccta cactctgagc agtcagtgatc ctgtccctc cagcacctgg | 600 |
| cccagcgaga ccgtcacctg caacgttgcc cacccggcca gcagcaccaa ggtggacaag | 660 |
| aaaatttgtc ccagggattt tggttgtaa ccttgcataat gtacagtccc agaagtatca | 720 |
| tctgtttca tttttttttt aaagcccaag gatgtgtca ccattactt gactcctaag | 780 |
| gtcacgtgtt ttgtgttgcata catcagcaag gatgtcccg aggtccagtt cagctggttt | 840 |
| gttagatgttggaggtgcacagactcgac acgcaacccc gggaggagca gttcaacagc | 900 |
| actttccgcgt cagtcagtgacttccatc atgcaccagg actgggtcaa tggcaaggag | 960 |
| ttcaaattgtca gggtaaacatc tgcaatccatc cctggcccaatc tggaaaaac catctccaa | 1020 |
| accaaaggca gaccgaaggc tccacagggt tacaccatttccatc caccccccggagcagat | 1080 |
| gccaaaggata aagtcaatgtt gacatgttgcata ataacagact tttccctgtca agacattact | 1140 |
| gtggagtggc agtggaaatgg gcagccagcg gagaactaca agaacaactca gcccattat | 1200 |
| gacacagatg gcttttactt cgttctacagc aagctcaatgt tgcagaagag caactgggg | 1260 |
| gcaggaaata ctttcacctg ctctgtgtta catgaggggc tgcacaacca ccatactgag | 1320 |
| aagagcctct cccactctcc tggtaaatga | 1350 |

<210> SEQ ID NO 37

<211> LENGTH: 468

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 37

| | |
|---|--|
| Met Gly Arg Leu Thr Ser Ser Phe Leu Leu Ile Val Pro Ala Tyr | |
| 1 5 10 15 | |

| | |
|---|--|
| Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln | |
| 20 25 30 | |

Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu

-continued

| 35 | 40 | 45 |
|---|-----|-----|
| Ser Thr Ser Gly Met Gly Val Gly Trp Ile Arg His Pro Ser Gly Lys | | |
| 50 | 55 | 60 |
| Asn Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Val Lys Arg Tyr | | |
| 65 | 70 | 75 |
| Asn Pro Val Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Asn | | |
| 85 | 90 | 95 |
| Ser Gln Val Phe Leu Lys Ile Ala Asn Val Asp Thr Ala Asp Thr Ala | | |
| 100 | 105 | 110 |
| Thr Tyr Tyr Cys Ala Arg Ile Glu Asp Phe Asp Tyr Asp Glu Glu Tyr | | |
| 115 | 120 | 125 |
| Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Ile Val Ser Ser | | |
| 130 | 135 | 140 |
| Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala | | |
| 145 | 150 | 155 |
| 160 | | |
| Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr | | |
| 165 | 170 | 175 |
| Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser | | |
| 180 | 185 | 190 |
| Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu | | |
| 195 | 200 | 205 |
| Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val | | |
| 210 | 215 | 220 |
| Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys | | |
| 225 | 230 | 235 |
| 240 | | |
| Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro | | |
| 245 | 250 | 255 |
| Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu | | |
| 260 | 265 | 270 |
| Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser | | |
| 275 | 280 | 285 |
| Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu | | |
| 290 | 295 | 300 |
| Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr | | |
| 305 | 310 | 315 |
| 320 | | |
| Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn | | |
| 325 | 330 | 335 |
| Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro | | |
| 340 | 345 | 350 |
| Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln | | |
| 355 | 360 | 365 |
| Val Tyr Thr Ile Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val | | |
| 370 | 375 | 380 |
| Ser Leu Thr Cys Met Ile Thr Asp Phe Pro Glu Asp Ile Thr Val | | |
| 385 | 390 | 395 |
| 400 | | |
| Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln | | |
| 405 | 410 | 415 |
| Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn | | |
| 420 | 425 | 430 |
| Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val | | |
| 435 | 440 | 445 |
| Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His | | |
| 450 | 455 | 460 |

-continued

Ser Pro Gly Lys
465

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<210> SEQ ID NO 38
<211> LENGTH: 1407
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 38

atgggcaggc ttacttcttc attctgtcta ctgattgtcc ctgcataatgt cctgtccag 60
gttactctga aagagtctgg ccctggata ttgcagccct cccagaccct cagtctgact 120
tgttctttct ctgggttttc actgagcaact tctggatgg gtgttaggctg gattcgtcac 180
ccatcaggaa agaatctggaa gtggctggca cacatggatggatgt caagcgctat 240
aacccagttcc tgaagagccg actgactatc tccaaggata cctccaacag ccaggttattc
ctcaagatcg ccaatgtggaa cactgcagat actgccacat actactgtgc tcgaatagag 300
gactttgatt acgacgagga gtattatgct atggactact ggggtcaagg aacctcagtc 420
atcgcttcct cagccaaaac gacacccccc tctgtctatc cactggcccc tggatctgct 480
gcccaaacta actccatgggt gaccctggaa tgccctggta agggctatattt ccctgagcca 540
gtgacagtga cctggaaactc tggatccctg tccagcggtg tgcacacccccc 600
ctgcagtctg acctctacac tctgagcagc tcagtactg tccctccag cacctggccc 660
agcgagaccg tcacctgcaa cggtggccac cggccagca gcaccaaggt ggacaagaaa 720
attgtgccccca gggattgtgg ttgttaagcct tgcataatgtaa cagtcggaga agtacatct 780
gtcttcatct tcccccaaaa gcccaaggat gtgctcacca ttactctgac tcctaaggc 840
acgtgtgttg tggtagacat cagcaaggat gatcccgagg tccagttcag ctggttgt 900
gatgatgtgg aggtgcacac agctcagacg caaccccgagg aggagcgtt caacagcact 960
ttccgctcag tcagtgaaact tcccatcatg caccaggact ggctcaatgg caaggagttc
aaatgcaggg tcaacagtgc agcttccct gccccatcg agaaaaccat ctccaaaacc 1080
aaaggccagac cgaaggctcc acagggtgtac accattccac ctcccaagga gcagatggcc 1140
aaggataaaag tcagtgac ctgcataactt acagacttct tccctgaaga cattactgt 1200
gagtgccagt ggaatggca gccagcgagg aactacaaga acactcagcc catcatggac 1260
acagatggct cttacttcgt ctacagcaag ctcaatgtgc agaagagcaa ctggaggca 1320
ggaaataactt tcacctgctc tggatggcaat gggccctgc acaaccacca tactgagaag 1380
agcctctccc actctcctgg taaatga 1407

```

```

<210> SEQ ID NO 39
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

```

<400> SEQUENCE: 39

Asp His Tyr Met Ser
1 5

```

<210> SEQ ID NO 40
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

```

<400> SEQUENCE: 40

-continued

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Asn | Pro | Tyr | Ser | Gly | Glu | Thr | Thr | Tyr | Asn | Gln | Lys | Phe | Lys |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |

Gly

<210> SEQ ID NO 41
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 41

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Asp | Tyr | Asp | Ala | Ser | Pro | Phe | Ala | Tyr |
| 1 | | | 5 | | | | | 10 | |

<210> SEQ ID NO 42
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 42

| | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ala | Ser | Gln | Gly | Thr | Ser | Ile | Asn | Leu | Asn |
| 1 | | | 5 | | | | | 10 | | |

<210> SEQ ID NO 43
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 43

| | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ser | Ser | Asn | Leu | Glu | Asp |
| 1 | | | 5 | | | |

<210> SEQ ID NO 44
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 44

| | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gln | His | Ser | Tyr | Leu | Pro | Tyr | Thr |
| 1 | | | 5 | | | | | |

<210> SEQ ID NO 45
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 45

| | | | | |
|-----|-----|-----|-----|-----|
| Asp | Cys | Tyr | Met | Asn |
| 1 | | | 5 | |

<210> SEQ ID NO 46
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 46

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Asn | Pro | Phe | Asn | Gly | Gly | Thr | Thr | Tyr | Asn | Gln | Lys | Phe | Lys |
| 1 | | | | 5 | | | | 10 | | | | 15 | | | |

Gly

<210> SEQ ID NO 47
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

-continued

<400> SEQUENCE: 47

| | | |
|---|---|----|
| Ser His Tyr Tyr Phe Asp Gly Arg Val Pro Trp Asp Ala Met Asp Tyr | | |
| 1 | 5 | 10 |
| | | 15 |

<210> SEQ_ID NO 48

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 48

| | | |
|---|---|----|
| Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn | | |
| 1 | 5 | 10 |
| | | 15 |

<210> SEQ_ID NO 49

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 49

| | | |
|-----------------------------|---|--|
| Ala Ala Ser Asn Leu Glu Ser | | |
| 1 | 5 | |

<210> SEQ_ID NO 50

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 50

| | | |
|-------------------------------------|---|--|
| Gln Gln Ser Asn Glu Asp Pro Trp Thr | | |
| 1 | 5 | |

<210> SEQ_ID NO 51

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: Rabbit-mouse chimera

<400> SEQUENCE: 51

| | | |
|---------------------|---|--|
| Ser Tyr Trp Met Asn | | |
| 1 | 5 | |

<210> SEQ_ID NO 52

<211> LENGTH: 16

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: Rabbit-mouse chimera

<400> SEQUENCE: 52

| | | |
|---|---|----|
| Thr Ile Asp Ser Gly Gly Arg Thr Asp Tyr Ala Ser Trp Ala Lys Gly | | |
| 1 | 5 | 10 |
| | | 15 |

<210> SEQ_ID NO 53

<211> LENGTH: 4

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

-continued

<223> OTHER INFORMATION: Rabbit-Mouse chimera

<400> SEQUENCE: 53

Asn Trp Asn Leu
1

<210> SEQ ID NO 54
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Rabbit-mouse chimera

<400> SEQUENCE: 54

Gln Ser Ser Gln Ser Val Tyr Asp Asn Asn Trp Leu Ala
1 5 10

<210> SEQ ID NO 55
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Rabbit-mouse chimera

<400> SEQUENCE: 55

Asp Ala Ser Asp Leu Ala Ser
1 5

<210> SEQ ID NO 56
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Rabbit-mouse chimera

<400> SEQUENCE: 56

Gln Gly Ala Tyr Asn Asp Val Ile Tyr Ala
1 5 10

<210> SEQ ID NO 57
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 57

Thr Ser Gly Met Gly Val Gly
1 5

<210> SEQ ID NO 58
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 58

His Ile Trp Trp Asp Asp Val Lys Arg Tyr Asn Pro Val Leu Lys Ser
1 5 10 15

<210> SEQ ID NO 59

-continued

<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 59

Glu Asp Phe Asp Tyr Asp Glu Glu Tyr Tyr Ala Met Asp Tyr
1 5 10

<210> SEQ ID NO 60
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 60

Ser Ala Ser Ser Ser Val Ser Phe Val Asp
1 5 10

<210> SEQ ID NO 61
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 61

Arg Thr Ser Asn Leu Gly Phe
1 5

<210> SEQ ID NO 62
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 62

Gln Gln Arg Ser Thr Tyr Pro Pro Thr
1 5

<210> SEQ ID NO 63
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 63

Cys Gly Pro Ala Arg Leu Leu Pro Asn Ala Ile Gly Arg Gly Lys Trp
1 5 10 15

Trp Arg Pro Ser
20

<210> SEQ ID NO 64
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 64

Gly Pro Ala Arg Leu Leu Pro Asn Ala Ile Gly Arg Gly Lys Trp Trp
1 5 10 15

Arg Pro Ser Gly
20

<210> SEQ ID NO 65
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 65

Pro Ala Arg Leu Leu Pro Asn Ala Ile Gly Arg Gly Lys Trp Trp Arg

| | | | |
|---|---|----|----|
| 1 | 5 | 10 | 15 |
|---|---|----|----|

Pro Ser Gly Pro
20

<210> SEQ ID NO 66
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 66
Ala Arg Leu Leu Pro Asn Ala Ile Gly Arg Gly Lys Trp Trp Arg Pro
1 5 10 15

Ser Gly Pro Asp
20

<210> SEQ ID NO 67
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 67
Arg Leu Leu Pro Asn Ala Ile Gly Arg Gly Lys Trp Trp Arg Pro Ser
1 5 10 15

Gly Pro Asp Phe
20

<210> SEQ ID NO 68
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 68
Leu Leu Pro Asn Ala Ile Gly Arg Gly Lys Trp Trp Arg Pro Ser Gly
1 5 10 15

Pro Asp Phe Arg
20

<210> SEQ ID NO 69
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 69
Leu Pro Asn Ala Ile Gly Arg Gly Lys Trp Trp Arg Pro Ser Gly Pro
1 5 10 15

Asp Phe Arg Cys
20

<210> SEQ ID NO 70
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 70
Ser Ala Lys Pro Val Thr Glu Leu Val Cys Ser Gly Gln Cys
1 5 10

<210> SEQ ID NO 71
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 71

-continued

Leu Val Ala Ser Cys Lys Cys
1 5

<210> SEQ ID NO 72
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 72

Cys Arg Glu Leu His Phe Thr Arg
1 5

<210> SEQ ID NO 73
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 73

Cys Ile Pro Asp Arg Tyr Arg
1 5

<210> SEQ ID NO 74
<211> LENGTH: 399
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 74

| | | | | | | |
|------------|------------|-------------|-------------|-------------|------------|-----|
| atggacacga | gggcccccac | tcaagtgcgt | gggctcctgc | tgctctggct | cccgagggcc | 60 |
| acatttgctc | aagttctgac | ccagagtcca | agcagtctct | ccgcccagcgt | aggcgatcgt | 120 |
| gtgactatta | cctgtcaatc | tagtcagac | gtgtatgata | acaattggct | ggcgtggta | 180 |
| cagcaaaaac | cgggcaaagc | cccgaaagctg | ctcatctatg | acgcgtccga | tctggctagc | 240 |
| ggtgtgccaa | cccgttttag | tggcagtggc | agcggtaactg | actttaccct | cacaatttcg | 300 |
| tctctccagc | cggaagattt | cgccacttac | tattgtcaag | gtgcttacaa | cgatgtgatt | 360 |
| tatgccttcg | gtcaggcac | taaaagtagaa | atcaaacgt | | | 399 |

<210> SEQ ID NO 75
<211> LENGTH: 133
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 75

Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp
1 5 10 15

Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ser Ser
35 40 45

Gln Ser Val Tyr Asp Asn Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro
50 55 60

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asp Leu Ala Ser

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| | | | |
|---|-----|-----|----|
| 65 | 70 | 75 | 80 |
| Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr | | | |
| 85 | 90 | 95 | |
| Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys | | | |
| 100 | 105 | 110 | |
| Gln Gly Ala Tyr Asn Asp Val Ile Tyr Ala Phe Gly Gln Gly Thr Lys | | | |
| 115 | 120 | 125 | |
| Val Glu Ile Lys Arg | | | |
| 130 | | | |

<210> SEQ ID NO 76
<211> LENGTH: 393
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 76

| | |
|--|-----|
| atggagactg ggctgcgtg gtttcctg gtgcgtgtgc tcaaaggtgtt ccactgttag | 60 |
| gtgcagctgt tggagtctgg aggccccctt gtccacgttg gagggagctt gcgtttctct | 120 |
| tgtcagcaaa cccgttttccat cttatccctt tactggatgat attgggttgcgc cccggcacct | 180 |
| gggaaggggcc tggagtgggt gggcaccattt gattccggag gcccgtacaga ctacgcgtct | 240 |
| tggggcaaaagg gccgtttcac catttccgc gacaactcca aaaataccat gtacccatcg | 300 |
| atgaactctc tccgcgcaga ggacacagca cgtttattactt gtgcacgc aaatggatctg | 360 |
| tgggggtcaag gtactttgtt aacagtctcg agc | 393 |

<210> SEQ ID NO 77
<211> LENGTH: 131
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 77

| | | | |
|---|-----|-----|----|
| Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly | | | |
| 1 | 5 | 10 | 15 |
| Val His Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln | | | |
| 20 | 25 | 30 | |
| Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu | | | |
| 35 | 40 | 45 | |
| Ser Ser Tyr Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu | | | |
| 50 | 55 | 60 | |
| Glu Trp Val Gly Thr Ile Asp Ser Gly Gly Arg Thr Asp Tyr Ala Ser | | | |
| 65 | 70 | 75 | 80 |
| Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr | | | |
| 85 | 90 | 95 | |
| Met Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Arg Tyr | | | |
| 100 | 105 | 110 | |
| Tyr Cys Ala Arg Asn Trp Asn Leu Trp Gly Gln Gly Thr Leu Val Thr | | | |
| 115 | 120 | 125 | |
| Val Ser Ser | | | |

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130

<210> SEQ ID NO 78
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 78

Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> SEQ ID NO 79
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 79

Tyr Thr Ser Arg Leu Leu Ser
1 5

<210> SEQ ID NO 80
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 80

Gln Gln Gly Asp Thr Leu Pro Tyr Thr
1 5

<210> SEQ ID NO 81
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 81

Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> SEQ ID NO 82
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 82

Gln Gly Trp Gln Ala Phe Lys Asn Asp Ala Thr Glu Ile Ile Pro Gly
1 5 10 15

Leu Arg Glu Tyr Pro Glu Pro Pro
20

<210> SEQ ID NO 83
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 83

Thr Glu Ile Ile Pro Gly Leu Arg Glu Tyr Pro Glu Pro Pro Gln Glu
1 5 10 15

Leu Glu Asn Asn
20

<210> SEQ ID NO 84
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 84

| | | | | | | | | | | | | | | | |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Glu | Pro | Pro | Gln | Glu | Leu | Glu | Asn | Asn | Gln | Thr | Met | Asn | Arg | Ala |
| 1 | | | | 5 | | | | 10 | | | | 15 | | | |
| Glu Asn Gly Gly | | | | | | | | | | | | | | | |
| | | | | 20 | | | | | | | | | | | |

<210> SEQ_ID NO 85

<211> LENGTH: 20

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 85

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asn | Gly | Gly | Arg | Pro | Pro | His | His | Pro | Tyr | Asp | Thr | Lys | Asp | Val |
| 1 | | | | 5 | | | 10 | | | 15 | | | | | |

Ser Glu Tyr Ser

20

<210> SEQ_ID NO 86

<211> LENGTH: 14

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 86

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Cys | Arg | Glu | Leu | His | Tyr | Thr | Arg | Phe | Val | Thr | Asp | Gly | Pro | | |
| 1 | | | | 5 | | | 10 | | | | | | | | |

<210> SEQ_ID NO 87

<211> LENGTH: 25

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 87

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Arg | Glu | Leu | His | Tyr | Thr | Arg | Phe | Val | Thr | Asp | Gly | Pro | Ser | Arg |
| 1 | | | | 5 | | | 10 | | | 15 | | | | | |

Ser Ala Lys Pro Val Thr Glu Leu Val

20 25

<210> SEQ_ID NO 88

<211> LENGTH: 23

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 88

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Arg | Ser | Ala | Lys | Pro | Val | Thr | Glu | Leu | Val | Ser | Ser | Gly | Gln | Ser |
| 1 | | | | 5 | | | 10 | | | 15 | | | | | |

Gly Pro Arg Ala Arg Leu Leu

20

<210> SEQ_ID NO 89

<211> LENGTH: 25

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 89

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Gly | Pro | Ala | Arg | Leu | Leu | Pro | Asn | Ala | Ile | Gly | Arg | Val | Lys | Trp |
| 1 | | | | 5 | | | 10 | | | 15 | | | | | |

Trp Arg Pro Asn Gly Pro Asp Phe Arg

20 25

<210> SEQ_ID NO 90

<211> LENGTH: 20

US 9,089,553 B2

97

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<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 90

Arg Ala Gln Arg Val Gln Leu Leu Cys Pro Gly Gly Ala Ala Pro Arg
1 5 10 15

Ser Arg Lys Val
20

<210> SEQ_ID NO 91
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 91

Pro Gly Gly Ala Ala Pro Arg Ser Arg Lys Val Arg Leu Val Ala Ser
1 5 10 15

<210> SEQ_ID NO 92
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 92

Lys Arg Leu Thr Arg Phe His Asn Gln Ser Glu Leu Lys Asp Phe Gly
1 5 10 15

Pro Glu Thr Ala Arg Pro Gln
20

<210> SEQ_ID NO 93
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 93

Ile Pro Asp Arg Tyr Ala Gln Arg Val Gln Leu Leu Ser Pro Gly Gly
1 5 10 15

<210> SEQ_ID NO 94
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 94

Ser Glu Leu Lys Asp Phe Gly Pro Glu Thr Ala Arg Pro Gln Lys Gly
1 5 10 15

Arg Lys Pro Arg Pro Arg Ala Arg
20

<210> SEQ_ID NO 95
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 95

Lys Gly Arg Lys Pro Arg Pro Arg Ala Arg Gly Ala Lys Ala Asn Gln
1 5 10 15

Ala Glu Leu Glu Asn Ala Tyr
20

<210> SEQ_ID NO 96
<211> LENGTH: 18
<212> TYPE: PRT

98

US 9,089,553 B2

99**100**

-continued

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 96

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Asn | Ala | Ile | Gly | Arg | Val | Lys | Trp | Trp | Arg | Pro | Asn | Gly | Pro | Asp |
| 1 | | | | 5 | | 10 | | | | 15 | | | | | |

Phe Arg

<210> SEQ ID NO 97

<211> LENGTH: 22

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 97

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Trp | Trp | Arg | Pro | Asn | Gly | Pro | Asp | Phe | Arg | Cys | Ile | Pro | Asp | Arg |
| 1 | | | | 5 | | 10 | | | 15 | | | | | | |

| | | | | | |
|-----|-----|-----|-----|-----|-----|
| Tyr | Arg | Ala | Gln | Arg | Val |
| | | 20 | | | |

<210> SEQ ID NO 98

<211> LENGTH: 213

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 98

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Leu | Ser | Leu | Ala | Pro | Cys | Leu | Ala | Cys | Leu | Leu | Val | His | Ala |
| 1 | | | | | | 5 | | 10 | | 15 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Phe | Val | Ala | Val | Glu | Ser | Gln | Gly | Trp | Gln | Ala | Phe | Lys | Asn | Asp |
| | | 20 | | | 25 | | | | 30 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Thr | Glu | Ile | Ile | Pro | Gly | Leu | Arg | Glu | Tyr | Pro | Glu | Pro | Pro | Gln |
| | | 35 | | | 40 | | | 45 | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Leu | Glu | Asn | Asn | Gln | Thr | Met | Asn | Arg | Ala | Glu | Asn | Gly | Gly | Arg |
| | | 50 | | | 55 | | | 60 | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | His | His | Pro | Tyr | Asp | Thr | Lys | Asp | Val | Ser | Glu | Tyr | Ser | Cys |
| 65 | | | | | 70 | | | 75 | | 80 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Glu | Leu | His | Tyr | Thr | Arg | Phe | Val | Thr | Asp | Gly | Pro | Cys | Arg | Ser |
| | | | | | 85 | | | 90 | | 95 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Lys | Pro | Val | Thr | Glu | Leu | Val | Cys | Ser | Gly | Gln | Cys | Gly | Pro | Ala |
| | | | | | 100 | | | 105 | | 110 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Leu | Leu | Pro | Asn | Ala | Ile | Gly | Arg | Val | Lys | Trp | Trp | Arg | Pro | Asn |
| | | | | | | 115 | | 120 | | 125 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Asp | Phe | Arg | Cys | Ile | Pro | Asp | Arg | Tyr | Arg | Ala | Gln | Arg | Val |
| | | | | | 130 | | | 135 | | 140 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Leu | Leu | Cys | Pro | Gly | Gly | Ala | Ala | Pro | Arg | Ser | Arg | Lys | Val | Arg |
| 145 | | | | | 150 | | | 155 | | 160 | | | | | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Ala | Ser | Cys | Cys | Lys | Arg | Leu | Thr | Arg | Phe | His | Asn | Gln |
| | | | | | 165 | | | 170 | | 175 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Glu | Leu | Lys | Asp | Phe | Gly | Pro | Glu | Thr | Ala | Arg | Pro | Gln | Lys | Gly |
| | | | | | 180 | | | 185 | | 190 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Lys | Pro | Arg | Pro | Arg | Ala | Arg | Gly | Ala | Lys | Ala | Asn | Gln | Ala | Glu |
| | | | | | 195 | | | 200 | | 205 | | | | | |

| | | | | |
|-----|-----|-----|-----|-----|
| Leu | Glu | Asn | Ala | Tyr |
| | | 210 | | |

<210> SEQ ID NO 99

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

US 9,089,553 B2

101**102**

-continued

<400> SEQUENCE: 99

Tyr Thr Ser Arg Leu His Ser
1 5

<210> SEQ_ID NO 100

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 100

Gln Gln Gly Asp Thr Leu Pro Tyr Thr
1 5

<210> SEQ_ID NO 101

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 101

Arg Ala Ser Gln Val Ile Thr Asn Tyr Leu Tyr
1 5 10

<210> SEQ_ID NO 102

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 102

Tyr Thr Ser Arg Leu His Ser
1 5

<210> SEQ_ID NO 103

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 103

Gln Gln Gly Asp Thr Leu Pro Tyr Thr
1 5

<210> SEQ_ID NO 104

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 104

Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> SEQ_ID NO 105

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 105

Tyr Thr Ser Arg Leu Leu Ser
1 5

<210> SEQ_ID NO 106

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 106

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Gln Gln Gly Asp Thr Leu Pro Tyr Thr
1 5

<210> SEQ ID NO 107
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 107

Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> SEQ ID NO 108
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 108

Tyr Thr Ser Arg Leu Phe Ser
1 5

<210> SEQ ID NO 109
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 109

Gln Gln Gly Asp Thr Leu Pro Tyr Thr
1 5

<210> SEQ ID NO 110
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 110

Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> SEQ ID NO 111
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 111

Tyr Thr Ser Arg Leu Leu Ser
1 5

<210> SEQ ID NO 112
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 112

Gln Gln Gly Asp Thr Leu Pro Tyr Thr
1 5

<210> SEQ ID NO 113
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 113

Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

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<210> SEQ_ID NO 114
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 114

Tyr Thr Ser Thr Leu Gln Ser
1 5

<210> SEQ_ID NO 115
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 115

Gln Gln Gly Asp Thr Leu Pro Tyr Thr
1 5

<210> SEQ_ID NO 116
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 116

Ser Val Ser Ser Ser Ile Ser Ser Ser Asn Leu His
1 5 10

<210> SEQ_ID NO 117
<211> LENGTH: 213
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 117

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Thr Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Tyr Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Thr Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asp Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala Pro
100 105 110

Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly
115 120 125

Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn
130 135 140

Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn
145 150 155 160

Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
165 170 175

Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr
180 185 190

Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe

US 9,089,553 B2

107

108

-continued

195 200 205

Asn Arg Asn Glu Cys
210

<210> SEQ ID NO 118
<211> LENGTH: 642
<212> TYPE: DNA
<213> ORGANISM: *Mus musculus*

<400> SEQUENCE: 118

caaattgttc tctcccaagtc tccagcaatc ctgtctacat ctccaggggga gaaggtcaca 60
atgacttgca gggccagctc aagtgtatat tacatgcact ggtaccagca gaagccagga 120
tccctccccca aaccctggat ttatgccaca tccaacctgg cttctggagt ccctgttgc 180
ttcagtgccca gtgggtctgg gacctttac tctctcacaa tcaccagagt ggaggctgaa 240
gatgtgcgccca cttattactg ccagcagtgg agtagtgacc cactcacgtt cggtgctgg 300
accaagctgg agctgaaaacg ggctgatgt gcaccaactg tatccatctt cccaccatcc 360
agtgagcagt taacatctgg aggtgcctca gtctgtgtc tcttgaacaa cttctacccc 420
aaagacatca atgtcaagtg gaagattgat ggcagtgaac gacaaaatgg cgtcctgaac 480
agttggactg atcaggacag caaagacagc acctacagca tgagcagcac cctcacgttg 540
accaaggacg agtatgaacg acataacagc tataacctgtg aggccactca caagacatca 600
acttcaccca ttgtcaagag cttcaacagg aatgagttt ag 642

<210> SEQ_ID NO 119
<211> LENGTH: 235
<212> TYPE: PRT
<213> ORGANISM: *Mus musculus*

<400> SEQUENCE: 119

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Phe | Gln | Val | Gln | Ile | Phe | Ser | Phe | Leu | Leu | Ile | Ser | Ala | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30

Leu Ser Thr Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45

Ser Ser Val Tyr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60

Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80

Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95

Thr Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Tyr Cys Gln Gln Trp
100 105 110

Ser Ser Asp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125

Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
130 135 140

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
145 150 155 160 165 170

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser

US 9,089,553 B2

109**110**

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Tyr | Ser | Met | Ser | Ser | Thr | Leu | Thr | Leu | Thr | Lys | Asp | Glu | Tyr | Glu |
| 195 | | | | | | 200 | | | | | 205 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | His | Asn | Ser | Tyr | Thr | Cys | Glu | Ala | Thr | His | Lys | Thr | Ser | Thr | Ser |
| 210 | | | | | 215 | | | | | 220 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|
| Pro | Ile | Val | Lys | Ser | Phe | Asn | Arg | Asn | Glu | Cys | | | | | |
| 225 | | | | | 230 | | | | 235 | | | | | | |

<210> SEQ ID NO 120

<211> LENGTH: 708

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 120

| | | | | | | | | | | |
|-------------|-------------|-------------|------------|------------|------------|-----|-------|-------|------------|-----|
| atggatttcc | aagtgcagat | tttcagcttc | ctgctaata | ca | gtgc | tta | gttca | gttcc | cattatgtcc | 60 |
| agggggacaaa | ttgttctctc | ccaggcttcca | gcaatcctgt | ctacatctcc | aggggagaag | | | | | 120 |
| gtcacaatga | cttgccagggc | cagctcaagt | gtatattaca | tgcactggta | ccagcagaag | | | | | 180 |
| ccaggatcct | cccccaaaacc | ctggatttat | gccacatcca | acctggcttc | tggagtccct | | | | | 240 |
| gttcgcttca | gtggcagtgg | gtctgggacc | tcttactctc | tcacaatcac | cagagtggag | | | | | 300 |
| gtcgaagatg | ctgcccactta | ttactgccag | cagtggagta | gtgaccact | cacgttcgg | | | | | 360 |
| gttgggacca | agctggagct | gaaacgggct | gatgctgcac | caactgtatc | catcttccca | | | | | 420 |
| ccatccagtg | agcagttAAC | atctggaggt | gcctcagtcg | tgtgcttctt | gaacaacttc | | | | | 480 |
| taccccaaag | acatcaatgt | caagtggaa | attgatggca | gtgaacgaca | aaatggcg | | | | | 540 |
| ctgaacacgtt | ggactgtatca | ggacagcaaa | gacagcacct | acagcatgag | cagcaccc | | | | | 600 |
| acgttgcacca | aggacgagta | tgaacgacat | aacagctata | cctgtgaggc | cactcacaag | | | | | 660 |
| acatcaacctt | cacccattgt | caagagcttc | aacaggaatg | agtgttag | | | | | | 708 |

<210> SEQ ID NO 121

<211> LENGTH: 445

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 121

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Val | Gln | Gln | Ser | Gly | Pro | Glu | Leu | Val | Lys | Pro | Gly | Ala |
| 1 | | | | | 5 | | | 10 | | | 15 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Lys | Leu | Ser | Cys | Thr | Ala | Ser | Gly | Phe | Asn | Ile | Lys | Asp | Tyr |
| | | | | | 20 | | | 25 | | | 30 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ile | His | Trp | Val | Lys | Gln | Arg | Pro | Glu | Gln | Gly | Leu | Glu | Trp | Ile |
| | | | | | 35 | | | 40 | | | 45 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Arg | Leu | Asp | Pro | Glu | Asp | Gly | Glu | Ser | Asp | Tyr | Ala | Pro | Lys | Phe |
| | | | | | 50 | | | 55 | | | 60 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Asp | Lys | Ala | Ile | Met | Thr | Ala | Asp | Thr | Ser | Ser | Asn | Thr | Ala | Tyr |
| | | | | | 65 | | | 70 | | | 75 | | | | 80 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gln | Leu | Arg | Ser | Leu | Thr | Ser | Glu | Asp | Thr | Ala | Ile | Tyr | Tyr | Cys |
| | | | | | 85 | | | 90 | | | 95 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Arg | Glu | Asp | Tyr | Asp | Gly | Thr | Tyr | Thr | Phe | Phe | Pro | Tyr | Trp | Gly |
| | | | | | 100 | | | 105 | | | 110 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Gly | Thr | Leu | Val | Thr | Val | Ser | Ala | Ala | Lys | Thr | Thr | Pro | Pro | Ser |
| | | | | | 115 | | | 120 | | | 125 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Pro | Leu | Ala | Pro | Gly | Ser | Ala | Ala | Gln | Thr | Asn | Ser | Met | Val |
| | | | | | 130 | | | 135 | | | 140 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Gly | Cys | Leu | Val | Lys | Gly | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val |
| | | | | | 145 | | | 150 | | | 155 | | | | 160 |

-continued

Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro
 180 185 190
 Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro
 195 200 205
 Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
 210 215 220
 Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile
 225 230 235 240
 Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys
 245 250 255
 Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln
 260 265 270
 Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln
 275 280 285
 Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu
 290 295 300
 Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg
 305 310 315 320
 Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 325 330 335
 Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro
 340 345 350
 Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr
 355 360 365
 Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
 370 375 380
 Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly
 385 390 395 400
 Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu
 405 410 415
 Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn
 420 425 430
 His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 435 440 445

<210> SEQ_ID NO 122
 <211> LENGTH: 1338
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 122

```

gagggttcagg tgcagcagtc tgggccagaa cttgtgaagc caggggccctc agtcaagttg      60
tcttgccacag ttctctggctt caacataaaa gactactta tacactgggt gaagcagagg      120
cctgaacagg gcctggagtg gatttggaaagg ctgtatctg aggatggtga aagtgttat      180
gccccgaagt tccaggacaa ggccattatg acagcagaca catcatccaa cacagcctat      240
cttcagctca gaagcctgac atctgaggac actgcccattt attattgtga gagagaggac      300
tacgtggta octacacctt ttttccttac tggggccaag ggactctggt cactgtctct      360
gcagccaaaa cgacacccccc atctgtctat ccactggccc ctggatctgc tgcccaaact      420
aactccatgg tgaccctggg atgcctggtc aagggttattt tccctgagcc agtgcacagt      480
acctggaaact ctggatccct gtccagcggt gtgcacaccc tcccaactgt cctgcagtc      540

```

-continued

| | |
|--|------|
| gacctctaca ctctgagcag ctcagtact gtcacccctcca gcacctggcc cagcgagacc | 600 |
| gtcacctgca acgttgcaca cccggccagc agcaccaagg tggacaagaa aatttgtcccc | 660 |
| agggattgtg gttgttaagcc ttgcataatgt acagtcggc aagtatcatc tgtcttcattc | 720 |
| tcccccggaa agcccaagga tggcttcacc attactctga ctcctaaggt cacgtgtgtt | 780 |
| gtggtagaca tcagcaagga tgatcccgag gtccagttca gctggttgt agatgtatgt | 840 |
| gaggtgcaca cagtcagac gcaaccccg gaggagcgt tcaacagcac tttccgctca | 900 |
| gtcagtgaac ttccatcat gcaccaggac tggctcaatg gcaaggagtt caaatgcagg | 960 |
| gtcaacatgt cagcttcccc tgccccatc gagaaaaacc tctccaaaac caaaggcaga | 1020 |
| ccgaaggctc cacaggtgtt caccattcca cttcccaagg agcagatggc caaggataaa | 1080 |
| gtcagtctga octgcatgtat aacagacttc ttccctgtt gacattactgt ggagtggcag | 1140 |
| tggaatgggc agccagcggg gaactacaag aacactcagc ccatcatggc cacagatggc | 1200 |
| tcttacttca tctacagcaa gctcaatgtg cagaagagca actggggagggc aggaaataact | 1260 |
| ttcacctgct ctgtgttaca tgagggcttg cacaaccacc atactgagaa gagcctctcc | 1320 |
| cactctctg gttaatgt | 1338 |

<210> SEQ ID NO 123

<211> LENGTH: 464

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 123

| | |
|---|--|
| Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly | |
| 1 5 10 15 | |

| | |
|---|--|
| Val Asn Ser Glu Val Gln Val Gln Ser Gly Pro Glu Leu Val Lys | |
| 20 25 30 | |

| | |
|---|--|
| Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile | |
| 35 40 45 | |

| | |
|---|--|
| Lys Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu | |
| 50 55 60 | |

| | |
|---|--|
| Glu Trp Ile Gly Arg Leu Asp Pro Glu Asp Gly Glu Ser Asp Tyr Ala | |
| 65 70 75 80 | |

| | |
|---|--|
| Pro Lys Phe Gln Asp Lys Ala Ile Met Thr Ala Asp Thr Ser Ser Asn | |
| 85 90 95 | |

| | |
|---|--|
| Thr Ala Tyr Leu Gln Leu Arg Ser Leu Thr Ser Glu Asp Thr Ala Ile | |
| 100 105 110 | |

| | |
|---|--|
| Tyr Tyr Cys Glu Arg Glu Asp Tyr Asp Gly Thr Tyr Thr Phe Phe Pro | |
| 115 120 125 | |

| | |
|---|--|
| Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr | |
| 130 135 140 | |

| | |
|---|--|
| Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn | |
| 145 150 155 160 | |

| | |
|---|--|
| Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro | |
| 165 170 175 | |

| | |
|---|--|
| Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr | |
| 180 185 190 | |

| | |
|---|--|
| Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val | |
| 195 200 205 | |

| | |
|---|--|
| Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val | |
| 210 215 220 | |

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Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg
 225 230 235 240
 Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser
 245 250 255
 Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu
 260 265 270
 Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro
 275 280 285
 Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala
 290 295 300
 Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val
 305 310 315 320
 Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe
 325 330 335
 Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr
 340 345 350
 Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile
 355 360 365
 Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys
 370 375 380
 Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp
 385 390 395 400
 Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp
 405 410 415
 Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser
 420 425 430
 Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly
 435 440 445
 Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 450 455 460

<210> SEQ ID NO 124
 <211> LENGTH: 1395
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 124

```

atgaaatgca gctgggtcat cttttcctg atggcagtgg ttacaggggt caattcagag   60
gttcagggtgc agcagtctgg gccagaacctt gtgaagccag gggcctcagt caagttgtcc 120
tgcacagctt ctggcttcaa cattaaagac tactttatac actgggtgaa gcagaggcct 180
gaacagggcc tggagtgat tggaaggctt gatcctgagg atggtaaaag tgattatgcc 240
ccgaagttcc aggacaaggc cattatgaca gcagacacat catccaacac agcctatctt 300
cagctcagaa gcctgacatc tgaggacact gccatctatt atttgtgagag agaggactac 360
gatggtacct acacccccatc tccttactgg ggccaaggga ctctggcac tgtctctgca 420
gccaaaaacga caccatccatc tgtcttatcca ctggccctcg gatctgctgc ccaaactaac 480
tccatggatc ccctggatc cctggtcaag ggctattcc ctgagccagt gacagtgacc 540
tggaaactctg gatccctgtc cagcggtgtc cacacccatc cagctgtctc gcagttgtac 600
ctctacatctc tgagcagctc agtgcactgtc ccctccagca cctggccctcg cgagaccgtc 660
acctgcaacg ttgcccaccc ggccagcagc accaagggtgg acaagaaaat tgtgcccagg 720
gattgtggtt gtaaggcttg catatgtaca gtcccagaag tatcatctgt cttcatcttc 780

```

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| | |
|--|------|
| cccccaaaggc ccaaggatgt gctaccattt actctgactc ctaaggtcac gtgtgttg | 840 |
| gttagacatca gcaaggatga tcccgaggtc cagttcagct ggtttgtaga tgatgtggag | 900 |
| gtgcacacag ctcagacgca accccggag gagcagttca acagcactt ccgctcagtc | 960 |
| agtgaacttc ccatcatgca ccaggactgg ctcaatggca aggagttcaa atgcagggtc | 1020 |
| aacagtgcag cttccctgc ccccatcgag aaaaccatct caaaaaccaa aggcagacccg | 1080 |
| aaggctccac aggtgtacac cattccacct cccaaggagc agatggccaa ggataaaagtc | 1140 |
| agtctgacct gcatgataac agacttcttc cctgaagaca ttactgtgga gtggcagtgg | 1200 |
| aatgggcagc cagcggagaa ctacaagaac actcagccca tcattggacac agatggctct | 1260 |
| tacttcatct acagcaagct caatgtgcag aagagcaact gggaggcagg aaatacttcc | 1320 |
| acctgctctg tgttacatga gggcctgcac aaccaccata ctgagaagag cctctccac | 1380 |
| tctcctggta aatga | 1395 |

<210> SEQ_ID NO 125

<211> LENGTH: 215

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 125

| | | | |
|---|---|----|----|
| Glu Ile Val Leu Thr Gln Ser Pro Ala Leu Met Ala Ala Ser Pro Gly | | | |
| 1 | 5 | 10 | 15 |

| | | | |
|---|----|----|--|
| Glu Lys Val Thr Ile Thr Cys Ser Val Ser Ser Thr Ile Ser Ser Asn | | | |
| 20 | 25 | 30 | |

| | | | |
|---|----|----|--|
| His Leu His Trp Phe Gln Gln Lys Ser Asp Thr Ser Pro Lys Pro Trp | | | |
| 35 | 40 | 45 | |

| | | | |
|---|----|----|--|
| Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser | | | |
| 50 | 55 | 60 | |

| | | | |
|---|----|----|----|
| Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu | | | |
| 65 | 70 | 75 | 80 |

| | | | |
|---|----|----|--|
| Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro | | | |
| 85 | 90 | 95 | |

| | | | |
|---|-----|-----|--|
| Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Arg Arg Ala Asp Ala | | | |
| 100 | 105 | 110 | |

| | | | |
|---|-----|-----|--|
| Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser | | | |
| 115 | 120 | 125 | |

| | | | |
|---|-----|-----|--|
| Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp | | | |
| 130 | 135 | 140 | |

| | | | |
|---|-----|-----|-----|
| Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val | | | |
| 145 | 150 | 155 | 160 |

| | | | |
|---|-----|-----|--|
| Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met | | | |
| 165 | 170 | 175 | |

| | | | |
|---|-----|-----|--|
| Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser | | | |
| 180 | 185 | 190 | |

| | | | |
|---|-----|-----|--|
| Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys | | | |
| 195 | 200 | 205 | |

| | | |
|-----------------------------|-----|--|
| Ser Phe Asn Arg Asn Glu Cys | | |
| 210 | 215 | |

<210> SEQ_ID NO 126

<211> LENGTH: 648

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 126

US 9,089,553 B2

119

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| | |
|--|-----|
| gaaaattgtgc tcacccagtc tccagcactc atggctgcat ctccggggga gaaggtcacc | 60 |
| atcacctgca gtgtcagtgc aactataagt tccaaccact tgcaactgggtt ccagcagaag | 120 |
| tcaagacacct ccccaaacc ctggatttat ggcacatcca acctggcttc tggagtccct | 180 |
| gttcgcttca gtggcagtgg atctgggacc tcttattctc tcacaatcag cagcatggag | 240 |
| gtcgaggatg ctgccactta ttactgtcaa cagtgagta gttacccact cacgttcggc | 300 |
| gtcgccacca agctggagct gagacgggct gatgctgcac caactgtatc catttccca | 360 |
| ccatccagtg agcagttAAC atctggaggt gcctcagtgc tggctttaa gaacaacttc | 420 |
| taccccaaaag acatcaatgt caagtggaaag attgatggca gtgaacgcaca aaatggcgtc | 480 |
| ctgaacagtt ggactgatca ggacagcaaa gacagcacct acagcatgag cagcacccctc | 540 |
| acgttgcacca aggacgagta tgaacgcacat aacagctata cctgtgaggc cactcacaag | 600 |
| acatcaactt cacccattgt caagagcttc aacaggaatg agtgttag | 648 |

<210> SEQ ID NO 127

<211> LENGTH: 237

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 127

| | | | |
|---|---|----|----|
| Met Asp Phe His Val Gln Ile Phe Ser Phe Met Leu Ile Ser Val Thr | | | |
| 1 | 5 | 10 | 15 |

| | | | |
|---|----|----|--|
| Val Ile Leu Ser Ser Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Leu | | | |
| 20 | 25 | 30 | |

| | | | |
|---|----|----|--|
| Met Ala Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Val Ser | | | |
| 35 | 40 | 45 | |

| | | | |
|---|----|----|--|
| Ser Thr Ile Ser Ser Asn His Leu His Trp Phe Gln Gln Lys Ser Asp | | | |
| 50 | 55 | 60 | |

| | | | |
|---|----|----|----|
| Thr Ser Pro Lys Pro Trp Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly | | | |
| 65 | 70 | 75 | 80 |

| | | | |
|---|----|----|--|
| Val Pro Val Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu | | | |
| 85 | 90 | 95 | |

| | | | |
|---|-----|-----|--|
| Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln | | | |
| 100 | 105 | 110 | |

| | | | |
|---|-----|-----|--|
| Gln Trp Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu | | | |
| 115 | 120 | 125 | |

| | | | |
|---|-----|-----|--|
| Leu Arg Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser | | | |
| 130 | 135 | 140 | |

| | | | |
|---|-----|-----|-----|
| Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn | | | |
| 145 | 150 | 155 | 160 |

| | | | |
|---|-----|-----|--|
| Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser | | | |
| 165 | 170 | 175 | |

| | | | |
|---|-----|-----|--|
| Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys | | | |
| 180 | 185 | 190 | |

| | | | |
|---|-----|-----|--|
| Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu | | | |
| 195 | 200 | 205 | |

| | | | |
|---|-----|-----|--|
| Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser | | | |
| 210 | 215 | 220 | |

| | | | |
|---|-----|-----|--|
| Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys | | | |
| 225 | 230 | 235 | |

<210> SEQ ID NO 128

<211> LENGTH: 714

120

-continued

<212> TYPE: DNA
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 128

```

atggatttccatgtcagat tttcagcttc atgctaatacgatgtcacatgc cattttgtcc      60
agtggagaaa ttgtgtcac ccagtctcca gcactcatgg ctgcacatctcc gggggagaag     120
gtcaccatca cctgcaggatgt cagttcaact ataagttcca accacttgca ctgggttccag     180
cagaagtcac acacccccc caaacccctgg atttatggca catccaacact ggcttctgga     240
gtccctgttc gcttcaggatgg cagttggatct gggaccttatttctcac aatcagcagc     300
atggaggctg aggtatgtc cacttattac tgtcaacatgtt ggagtagtta cccactcactg     360
ttcggegctg ggaccaagct ggagctgaga cgggctgtatgc ctgcaccaac tgcacatccatc   420
ttccccccat ccacgtgagca gttaacatct ggaggtgcct cagtcgtgtg cttttgaac     480
aacttctacc ccaaagacat caatgtcaag tggaaagatttgc atggcagtgaa acgacaaaat    540
ggcgtccatca acagttggac tgatcaggac agcaaagaca gcacccatcag catggcagc     600
accctcacatgttggatgg cggatgttgc cggatgttgc cggatgttgc cggatgttgc       660
cacaagacat caacttcacc cattgtcaag agcttcaaca ggaatggatgttgc ttag        714

```

<210> SEQ ID NO 129
 <211> LENGTH: 449
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 129

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Gln | Gln | Ser | Gly | Ala | Glu | Leu | Val | Arg | Pro | Gly | Ala |
| 1 | | | | | | | | | 10 | | | | | | 15 |
| Leu | Val | Lys | Leu | Ser | Cys | Thr | Ala | Ser | Asp | Phe | Asn | Ile | Lys | Asp | Phe |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| Tyr | Leu | His | Trp | Met | Arg | Gln | Arg | Pro | Glu | Gln | Gly | Leu | Asp | Trp | Ile |
| | | | | 35 | | | 40 | | | | 45 | | | | |
| Gly | Arg | Ile | Asp | Pro | Glu | Asn | Gly | Asp | Thr | Leu | Tyr | Asp | Pro | Lys | Phe |
| | | | | 50 | | | 55 | | | 60 | | | | | |
| Gln | Asp | Lys | Ala | Thr | Leu | Thr | Thr | Asp | Thr | Ser | Ser | Asn | Thr | Ala | Tyr |
| | | | | 65 | | | 70 | | | 75 | | | 80 | | |
| Leu | Gln | Leu | Ser | Gly | Leu | Thr | Ser | Glu | Thr | Thr | Ala | Val | Tyr | Tyr | Cys |
| | | | | | 85 | | | 90 | | | 95 | | | | |
| Ser | Arg | Glu | Ala | Asp | Tyr | Phe | His | Asp | Gly | Thr | Ser | Tyr | Trp | Tyr | Phe |
| | | | | 100 | | | 105 | | | 110 | | | | | |
| Asp | Val | Trp | Gly | Ala | Gly | Thr | Thr | Ile | Thr | Val | Ser | Ser | Ala | Lys | Thr |
| | | | | 115 | | | 120 | | | 125 | | | | | |
| Thr | Pro | Pro | Ser | Val | Tyr | Pro | Leu | Ala | Pro | Gly | Ser | Ala | Ala | Gln | Thr |
| | | | | 130 | | | 135 | | | 140 | | | | | |
| Asn | Ser | Met | Val | Thr | Leu | Gly | Cys | Leu | Val | Lys | Gly | Tyr | Phe | Pro | Glu |
| | | | | 145 | | | 150 | | | 155 | | | 160 | | |
| Pro | Val | Thr | Val | Thr | Trp | Asn | Ser | Gly | Ser | Leu | Ser | Ser | Gly | Val | His |
| | | | | 165 | | | 170 | | | 175 | | | | | |
| Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser | Asp | Leu | Tyr | Thr | Leu | Ser | Ser | Ser |
| | | | | 180 | | | 185 | | | 190 | | | | | |
| Val | Thr | Val | Pro | Ser | Ser | Thr | Trp | Pro | Ser | Glu | Thr | Val | Thr | Cys | Asn |
| | | | | 195 | | | 200 | | | 205 | | | | | |
| Val | Ala | His | Pro | Ala | Ser | Ser | Thr | Lys | Val | Asp | Lys | Lys | Ile | Val | Pro |
| | | | | 210 | | | 215 | | | 220 | | | | | |

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Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser
 225 230 235 240

 Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr
 245 250 255

 Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp
 260 265 270

 Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr
 275 280 285

 Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser
 290 295 300

 Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

 Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys
 325 330 335

 Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr
 340 345 350

 Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr
 355 360 365

 Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
 370 375 380

 Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
 385 390 395 400

 Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys
 405 410 415

 Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu
 420 425 430

 Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
 435 440 445

Lys

```

<210> SEQ_ID NO 130
<211> LENGTH: 1350
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 130

gagggttcagc tgcagcagtc tggggctgaa cttgtgaggc cagggggcctt agtcaagttg        60
tcctgcacag cttctgactt caacattaaa gacttctatc tacactggat gaggcagcgg        120
cctgaacagg gcctggactg gatttggaaagg attgtatcctg agaatgggtga tactttatat        180
gaccgcgaagt tccaggacaa ggccactttt acaacagaca catcctccaa cacagcctac        240
ctgcagctca gcggcgttac atctgagacc actggcgatc attactgttc tagagaggcg        300
gattatttcc acgtatggta ctcctactgg tacttcgtatg tctggggcgc agggaccaca        360
atcacccgtct cctcagccaa aacgacaccc ccatctgtct atccactggc ccctggatct        420
gtgtccccaa ctaactccat ggtgaccctg ggatgcctgg tcaagggccta ttcccctgag        480
ccagtgcacag tgacctggaa ctctggatcc ctgtccagcg gtgtgcacac cttcccaagct        540
gtcctgcagt ctgacacctta cactctgagc agtcagtgatc ctgtccccctc cagcacctgg        600
cccagcgaga ccgtcacctg caacgttgcc caccggccca gcagcaccaa ggtggacaag        660
aaaaattgtgc ccaggatttgg tggttgtaaag ccttgcataat gtacagtccc agaagtatca        720
tctgtcttca tcttcccccc aaagcccaag gatgtgtca ccattactct gactcttaag        780
gtcacgtgtg ttgtggtaga catcagcaag gatgatcccc aggtccagtt cagctggtt        840
  
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gttagatgtg tggaggtgca cacagctcg acgcaacccc gggaggagca gttcaacagc      900
actttccgc cagtcagtga acttccccatc atgcaccagg actggctcaa tggcaaggag      960
ttcaaatgca gggtaaacag tgcaagtttc cctgccccca tcgagaaaac catctccaaa     1020
accaaaggca gaccgaaggc tccacagggt tacaccattc cacctccaa ggagcagatg     1080
gccaaggata aagtcagtct gacctgcattg ataacagact tcttcctga agacattact     1140
gtggagtggc agtggaatgg gcagccagcg gagaactaca agaacactca gcccatcatg     1200
gacacagatg gctttactt catctacagc aagctcaatg tgcaagaagag caactggag     1260
gcaggaaata ctttcacctg ctctgtgtta catgagggcc tgcacaacca ccatactgag     1320
aagagcctct cccactctcc tggtaaatga                                         1350

```

<210> SEQ ID NO 131

<211> LENGTH: 468

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 131

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Cys | Ser | Trp | Val | Ile | Phe | Phe | Leu | Met | Ala | Val | Val | Thr | Gly |
| 1 | | | | | | | 5 | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Ser | Glu | Val | Gln | Leu | Gln | Ser | Gly | Ala | Glu | Leu | Val | Arg |
| | 20 | | | | | | | 25 | | | | | 30 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Ala | Leu | Val | Lys | Leu | Ser | Cys | Thr | Ala | Ser | Asp | Phe | Asn | Ile |
| | 35 | | | | | | 40 | | | | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asp | Phe | Tyr | Leu | His | Trp | Met | Arg | Gln | Arg | Pro | Glu | Gln | Gly | Leu |
| | 50 | | | | | | 55 | | | 60 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Trp | Ile | Gly | Arg | Ile | Asp | Pro | Glu | Asn | Gly | Asp | Thr | Leu | Tyr | Asp |
| 65 | | | | | | 70 | | | 75 | | | 80 | | | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Lys | Phe | Gln | Asp | Lys | Ala | Thr | Leu | Thr | Asp | Thr | Ser | Ser | Asn |
| | 85 | | | | | | 90 | | | 95 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Tyr | Leu | Gln | Leu | Ser | Gly | Leu | Thr | Ser | Glu | Thr | Thr | Ala | Val |
| | 100 | | | | | | | 105 | | | | 110 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Cys | Ser | Arg | Glu | Ala | Asp | Tyr | Phe | His | Asp | Gly | Thr | Ser | Tyr |
| 115 | | | | | | | 120 | | | 125 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Tyr | Phe | Asp | Val | Trp | Gly | Ala | Gly | Thr | Thr | Ile | Thr | Val | Ser | Ser |
| 130 | | | | | 135 | | | | 140 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Lys | Thr | Thr | Pro | Pro | Ser | Val | Tyr | Pro | Leu | Ala | Pro | Gly | Ser | Ala |
| 145 | | | | | 150 | | | | 155 | | | 160 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Thr | Asn | Ser | Met | Val | Thr | Leu | Gly | Cys | Leu | Val | Lys | Gly | Tyr |
| | 165 | | | | | | 170 | | | 175 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Pro | Glu | Pro | Val | Thr | Val | Thr | Trp | Asn | Ser | Gly | Ser | Leu | Ser | Ser |
| | 180 | | | | | | 185 | | | 190 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Val | His | Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser | Asp | Leu | Tyr | Thr | Leu |
| | 195 | | | | | | 200 | | | 205 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Ser | Val | Thr | Val | Pro | Ser | Ser | Thr | Trp | Pro | Ser | Glu | Thr | Val |
| 210 | | | | | 215 | | | | 220 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Cys | Asn | Val | Ala | His | Pro | Ala | Ser | Ser | Thr | Lys | Val | Asp | Lys | Lys |
| 225 | | | | | | 230 | | | 235 | | | 240 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Val | Pro | Arg | Asp | Cys | Gly | Cys | Lys | Pro | Cys | Ile | Cys | Thr | Val | Pro |
| 245 | | | | | | 250 | | | 255 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Ser | Ser | Val | Phe | Ile | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Val | Leu |
| | 260 | | | | | 265 | | | | 270 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Thr | Leu | Thr | Pro | Lys | Val | Thr | Cys | Val | Val | Val | Asp | Ile | Ser |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

US 9,089,553 B2

127

-continued

128

| 275 | 280 | 285 |
|---|-----|-----|
| Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu | | |
| 290 | 295 | 300 |
| Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr | | |
| 305 | 310 | 315 |
| Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn | | |
| 325 | 330 | 335 |
| Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro | | |
| 340 | 345 | 350 |
| Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln | | |
| 355 | 360 | 365 |
| Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val | | |
| 370 | 375 | 380 |
| Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val | | |
| 385 | 390 | 395 |
| Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln | | |
| 405 | 410 | 415 |
| Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn | | |
| 420 | 425 | 430 |
| Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val | | |
| 435 | 440 | 445 |
| Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His | | |
| 450 | 455 | 460 |
| Ser Pro Gly Lys | | |
| 465 | | |

<210> SEQ_ID NO 132
<211> LENGTH: 1407
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 132

| | |
|--|------|
| atgaaatgca gctgggtcat cttttccctg atggcagtgg ttacaggggt caattcagag | 60 |
| gttcagtcg acgactctgg ggctgaacctt gtgaggccag gggccttagt caagttgtcc | 120 |
| tgcacagctt ctgacttcaa cattaaagac ttctatctac actggatgag gcagccgcct | 180 |
| gaacaggccc tggactggat tggaggatt gatcctgaga atggatgatac ttttatatgac | 240 |
| ccgaagttcc aggacaaggc cactttaca acagacacat cctccaacac agcctacctg | 300 |
| cagctcagcg gcctgacatc tgagaccact gccgtctatt actgttctag agaggccgat | 360 |
| tattttcacg atggtaacctc ctactggatc ttctatgtct ggggcgcagg gaccacaatc | 420 |
| accgtctctt cagccaaaac gacacccca tctgtctatc cactggcccc tggatctgct | 480 |
| gcccaaacta actccatggt gaccctggga tgcctggta agggctattt ccctgagcca | 540 |
| gtgacagtga cctggaactc tggatccctg tccagcgggt tgccacaccc cccagctgtc | 600 |
| ctgcagtctg acctctacac tctgagcagc tcagtactg tccccctccag cacctggccc | 660 |
| agcgagaccc tcacctgcaa cggtccccac cccggccagca gcaccaaggt ggacaagaaa | 720 |
| atttgtccccca gggattgtgg ttgttaagcct tgcataatgtc cagtcccaga agtatacatct | 780 |
| gtcttcatct tccccccaaa gcccaaggat gtgctcacca ttactctgac tcctaaggtc | 840 |
| acgtgtgttg tggtagacat cagcaaggat gatcccagg tccagtttag ctgggttgc | 900 |
| gatgatgtgg aggtgcacac agctcagacg caaccccccggg aggagcaggta caacagcact | 960 |
| ttcccgctcg tcagtgact tcccatcatg caccaggact ggctcaatgg caaggagttc | 1020 |

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| | |
|--|------|
| aaatgcaggg tcaacagtgc agcttccct gccccatcg agaaaaccat ctccaaaacc | 1080 |
| aaaggcagac cgaaggctcc acagggtgtac accattccac ctcccaagga gcagatggcc | 1140 |
| aaggataaaag tcagtcgtac ctgcgtgata acagacttct tccctgaaga cattactgtg | 1200 |
| gagtggcagt ggaatgggca gccagcggag aactacaaga acactcagcc catcatggac | 1260 |
| acagatggct cttaacttcat ctacagcaag ctcaatgtgc agaagagcaa ctggaggca | 1320 |
| ggaataactt tcacctgctc tgtgttacat gagggcctgc acaaccacca tactgagaag | 1380 |
| agcctctccc actctcctgg taaatga | 1407 |

<210> SEQ ID NO 133

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 133

| | | | |
|---|---|----|----|
| Asp Ile Gln Met Thr Gln Ile Thr Ser Ser Leu Ser Ala Ser Leu Gly | | | |
| 1 | 5 | 10 | 15 |

| | | | |
|---|----|----|--|
| Asp Arg Val Ser Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr | | | |
| 20 | 25 | 30 | |

| | | | |
|---|----|----|--|
| Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe Lys Leu Leu Ile | | | |
| 35 | 40 | 45 | |

| | | | |
|---|----|----|--|
| Phe Tyr Thr Ser Arg Leu Leu Ser Gly Val Pro Ser Arg Phe Ser Gly | | | |
| 50 | 55 | 60 | |

| | | | |
|---|----|----|----|
| Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Tyr Asn Leu Glu Gln | | | |
| 65 | 70 | 75 | 80 |

| | | | |
|---|----|----|--|
| Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr | | | |
| 85 | 90 | 95 | |

| | | | |
|---|-----|-----|--|
| Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala | | | |
| 100 | 105 | 110 | |

| | | | |
|---|-----|-----|--|
| Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly | | | |
| 115 | 120 | 125 | |

| | | | |
|---|-----|-----|--|
| Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile | | | |
| 130 | 135 | 140 | |

| | | | |
|---|-----|-----|-----|
| Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu | | | |
| 145 | 150 | 155 | 160 |

| | | | |
|---|-----|-----|--|
| Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser | | | |
| 165 | 170 | 175 | |

| | | | |
|---|-----|-----|--|
| Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr | | | |
| 180 | 185 | 190 | |

| | | | |
|---|-----|-----|--|
| Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser | | | |
| 195 | 200 | 205 | |

| | |
|-------------------------|--|
| Phe Asn Arg Asn Glu Cys | |
| 210 | |

<210> SEQ ID NO 134

<211> LENGTH: 645

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 134

| | |
|---|----|
| gatatccaga tgacacagat tacatccctc ctgtctgcct ctctgggaga cagggtctcc | 60 |
|---|----|

| | |
|---|-----|
| atcagttgca gggcaagtca agacatttgc aatttttaa actggatca gcagaaacca | 120 |
|---|-----|

| | |
|--|-----|
| gatggaacctt ttaaactcct tatcttctac acatcaagat tactctcagg agtcccatca | 180 |
|--|-----|

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| | | |
|-----------------------------------|----------------------------------|-----|
| aggttcagtg gcagtgggtc tggAACAGAT | tattctctca ccatttacaa cctggagcaa | 240 |
| gaagatTTTG ccacttactt ttGCCAACAG | ggagatacgc ttccgtacac tttcgagggg | 300 |
| gggaccaAGC tggAAATAAA acgggctgat | gctgcaccaa ctgtatccat cttcccacca | 360 |
| tccagtGAGC agttaacatc tggaggtgcc | tcagtcgtgt gtttcttGAA caacttctac | 420 |
| ccaaAGACA tcaatgtcaa gtggAAGATT | gatggcAGTg aacgacAAAGA tggcgtctg | 480 |
| aacAGTTGGA ctgatcAGGA cagcaAAAGAC | agcacctaca gcatgAGCAG caccctcACG | 540 |
| ttgaccaAGG acgAGTATGA acgacataAC | agctataCCt gtgaggccAC tcacaAGAC | 600 |
| tcaacttcAC ccattgtCAA gagCTTCAC | aggaatgAGT gttAG | 645 |

<210> SEQ ID NO 135

<211> LENGTH: 234

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 135

| | | |
|---|-------------------------|--|
| Met Met Ser Ser Ala Gln Phe Leu Gly | Leu Leu Leu Cys Phe Gln | |
| 1 5 | 10 15 | |
| Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ile Thr Ser Ser | Leu Ser | |
| 20 25 | 30 | |
| Ala Ser Leu Gly Asp Arg Val Ser Ile Ser Cys Arg Ala Ser Gln Asp | | |
| 35 40 | 45 | |
| Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe | | |
| 50 55 | 60 | |
| Lys Leu Leu Ile Phe Tyr Thr Ser Arg Leu Leu Ser Gly Val Pro Ser | | |
| 65 70 | 75 80 | |
| Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Tyr | | |
| 85 90 | 95 | |
| Asn Leu Glu Gln Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asp | | |
| 100 105 | 110 | |
| Thr Leu Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg | | |
| 115 120 | 125 | |
| Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln | | |
| 130 135 | 140 | |
| Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr | | |
| 145 150 | 155 160 | |
| Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln | | |
| 165 170 | 175 | |
| Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr | | |
| 180 185 | 190 | |
| Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg | | |
| 195 200 | 205 | |
| His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro | | |
| 210 215 | 220 | |
| Ile Val Lys Ser Phe Asn Arg Asn Glu Cys | | |
| 225 230 | | |

<210> SEQ ID NO 136

<211> LENGTH: 705

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 136

atgatgtcct ctgctcagtt ccttgggttc ctgttgtctt gtttcaagg taccagatgt 60

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| | | |
|---|---------------------------------|-----|
| gatatccaga tgacacagat tacatcctcc | ctgtctgcct ctctggaga cagggtctcc | 120 |
| atcgatgc gggcaagtca agacatttc aattttaa actggatatac gcagaaacca | | 180 |
| gatggaaacctt ttaaactcct tatcttctac acatcaagat tactctcagg agtcccacca | | 240 |
| aggttcagtg gcagtggtc tggAACAGAT tattctctca ccatttacaa cctggagcaa | | 300 |
| gaagattttg ccacttactt ttgccaacag ggagatacgc ttccgtacac ttccggaggg | | 360 |
| gggaccaagc tggAAATAAA acgggctgtat gctgcaccaa ctgtatccat cttccacca | | 420 |
| tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gtttcttcaa caacttctac | | 480 |
| cccaaaagaca tcaatgtcaa gtggaaagatt gatggcagtg aacgacaaaa tggcgtctg | | 540 |
| aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcagc | | 600 |
| ttgaccaagg acgagttatga acgacataac agtataccat gtgaggccac tcacaagaca | | 660 |
| tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gttag | | 705 |

<210> SEQ_ID NO 137

<211> LENGTH: 447

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 137

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Gln | Gln | Ser | Gly | Pro | Glu | Leu | Met | Lys | Pro | Gly | Ala |
| 1 | | | | | | | | | 5 | | 10 | | | | 15 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Lys | Met | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe | Thr | Asp | Tyr |
| | | | | | | | | | 20 | | 25 | | | | 30 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Met | His | Trp | Val | Lys | Gln | Asn | Gln | Gly | Lys | Thr | Leu | Glu | Trp | Ile |
| | | | | | | | | | 35 | | 40 | | | | 45 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Glu | Ile | Asn | Pro | Asn | Ser | Gly | Gly | Ala | Gly | Tyr | Asn | Gln | Lys | Phe |
| | | | | | | | | 50 | | 55 | | | | | 60 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gly | Lys | Ala | Thr | Leu | Thr | Val | Asp | Lys | Ser | Ser | Thr | Thr | Ala | Tyr |
| | | | | | | | | 65 | | 70 | | | | | 80 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Arg | Ser | Leu | Thr | Ser | Glu | Asp | Ser | Ala | Val | Tyr | Tyr | Cys |
| | | | | | | | | 85 | | 90 | | | | | 95 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Arg | Leu | Gly | Tyr | Asp | Asp | Ile | Tyr | Asp | Asp | Trp | Tyr | Phe | Asp | Val |
| | | | | | | | 100 | | 105 | | | | | | 110 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Gly | Ala | Gly | Thr | Thr | Val | Thr | Val | Ser | Ser | Ala | Lys | Thr | Thr | Pro |
| | | | | | | | | 115 | | 120 | | | | | 125 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Val | Tyr | Pro | Leu | Ala | Pro | Gly | Ser | Ala | Ala | Gln | Thr | Asn | Ser |
| | | | | | | | | 130 | | 135 | | | | | 140 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Thr | Leu | Gly | Cys | Leu | Val | Lys | Gly | Tyr | Phe | Pro | Glu | Pro | Val |
| | | | | | | | | 145 | | 150 | | | | | 160 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Val | Thr | Trp | Asn | Ser | Gly | Ser | Leu | Ser | Ser | Gly | Val | His | Thr | Phe |
| | | | | | | | | 165 | | 170 | | | | | 175 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | Val | Leu | Gln | Ser | Asp | Leu | Tyr | Thr | Leu | Ser | Ser | Val | Thr | |
| | | | | | | | | 180 | | 185 | | | | | 190 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Ser | Ser | Thr | Trp | Pro | Ser | Glu | Thr | Val | Thr | Cys | Asn | Val | Ala |
| | | | | | | | | 195 | | 200 | | | | | 205 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Pro | Ala | Ser | Ser | Thr | Lys | Val | Asp | Lys | Lys | Ile | Val | Pro | Arg | Asp |
| | | | | | | | | 210 | | 215 | | | | | 220 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Gly | Cys | Lys | Pro | Cys | Ile | Cys | Thr | Val | Pro | Glu | Val | Ser | Ser | Val |
| | | | | | | | | 225 | | 230 | | | | | 240 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ile | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Val | Leu | Thr | Ile | Thr | Leu | Thr |
| | | | | | | | | 245 | | 250 | | | | | 255 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Pro | Lys | Val | Thr | Cys | Val | Val | Asp | Ile | Ser | Lys | Asp | Asp | Pro | Glu | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|

US 9,089,553 B2

135

136

-continued

| 260 | 265 | 270 |
|---|-----|-----|
| Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln | | |
| 275 | 280 | 285 |
| Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser | | |
| 290 | 295 | 300 |
| Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys | | |
| 305 | 310 | 315 |
| Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile | | |
| 325 | 330 | 335 |
| Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro | | |
| 340 | 345 | 350 |
| Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met | | |
| 355 | 360 | 365 |
| Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn | | |
| 370 | 375 | 380 |
| Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr | | |
| 385 | 390 | 395 |
| Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn | | |
| 405 | 410 | 415 |
| Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu | | |
| 420 | 425 | 430 |
| His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys | | |
| 435 | 440 | 445 |

<210> SEQ ID NO 138

<211> LENGTH: 1344

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 138

| | | | | | | |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| gagggtccaa | tgcacacagtc | tggacctgaa | ctaatacgtc | ctggggcttc | agtgaagatg | 60 |
| tcctgcagg | tttctggata | tacattcact | gactacaaca | tgcactgggt | gaagcagaac | 120 |
| caaggaaaga | cccttagatg | gataggagaa | attaatccta | acagtgggtt | tgctggctac | 180 |
| aaccagaagt | tcaagggcaa | ggccacattt | actgttagaca | agtccctcac | cacagcctac | 240 |
| atggagatcc | gcagectgac | atctgaggac | tctgcagtct | attactgtgc | aagattgggc | 300 |
| tacgatgata | tctacgacga | ctggtacttc | gatgtctggg | gcccggggac | cacggtcacc | 360 |
| gtctccctcg | ccaaaacgac | acccccatct | gtctatccac | tggcccttgg | atctgctgcc | 420 |
| caaactaact | ccatggtgac | cctgggatgc | ctggtaagg | gttatttccc | tgagccagtg | 480 |
| acagtgacct | ggaactctgg | atcccgttcc | agcgggtgtc | acaccttccc | agctgtctg | 540 |
| cagtctgacc | tctacactct | gaggactgtca | gtgactgtcc | cctccagcac | ctggcccagc | 600 |
| gagaccgtca | cctgcaacgt | tggccaccccg | gccagcagca | ccaagggttga | caagaaaatt | 660 |
| gtgcccagg | attgtggttt | taaggcttgc | atatgtacag | tcccagaagt | atcatctgtc | 720 |
| ttcatcttcc | ccccaaagcc | caaggatgtc | ctcaccattt | ctctgactcc | taaggtcacg | 780 |
| tgtgttgtgg | tagacatcg | caaggatgt | cccgagggtcc | agttcagctg | gtttgttagat | 840 |
| gatgtggagg | tgcacacagc | tcagacgca | ccccggggagg | agcagttcaa | cagcacttcc | 900 |
| cgctcagtca | gtgaacttcc | catcatgcac | caggactggc | tcaatggcaa | ggagttcaaa | 960 |
| tgcagggtca | acagtgcagc | tttccctgcc | cccatcgaga | aaaccatctc | caaaaccaaa | 1020 |
| ggcagaccga | aggctccaca | ggtgtacacc | attccacctc | ccaaggagca | gatggccaag | 1080 |

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gataaaagtca gtctgacctg catgataaca gacttcttcc ctgaagacat tactgtggag 1140
 tggcagtggaa atgggcagcc agcggagaac tacaagaaca ctcagccat catggacaca 1200
 gatggctt acttcatcta cagcaagctc aatgtgcaga agagcaactg ggaggcagga 1260
 aatactttca cctgtctgt gttacatgag ggcctgcaca accaccatac tgagaagagc 1320
 ctctcccact ctccctggtaa atga 1344

<210> SEQ ID NO 139

<211> LENGTH: 466

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 139

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Trp | Ser | Trp | Thr | Phe | Leu | Leu | Ser | Gly | Thr | Ala | Gly |
| 1 | | | | | | | 5 | | 10 | | 15 | | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ser | Glu | Val | Gln | Leu | Gln | Ser | Gly | Pro | Glu | Leu | Met | Lys |
| | | | | 20 | | | 25 | | | | 30 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Ala | Ser | Val | Lys | Met | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe |
| | | | | | | 35 | | 40 | | | 45 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asp | Tyr | Asn | Met | His | Trp | Val | Lys | Gln | Asn | Gln | Gly | Lys | Thr | Leu |
| | | | | | | 50 | | | 55 | | 60 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Trp | Ile | Gly | Glu | Ile | Asn | Pro | Asn | Ser | Gly | Gly | Ala | Gly | Tyr | Asn |
| | | | | | | 65 | | 70 | | 75 | | 80 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Lys | Phe | Lys | Gly | Lys | Ala | Thr | Leu | Thr | Val | Asp | Lys | Ser | Ser | Thr |
| | | | | | | 85 | | 90 | | | 95 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Tyr | Met | Glu | Leu | Arg | Ser | Leu | Thr | Ser | Glu | Asp | Ser | Ala | Val |
| | | | | | | 100 | | 105 | | | 110 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Cys | Ala | Arg | Leu | Gly | Tyr | Asp | Asp | Ile | Tyr | Asp | Asp | Trp | Tyr |
| | | | | | | 115 | | 120 | | 125 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Asp | Val | Trp | Gly | Ala | Gly | Thr | Thr | Val | Thr | Val | Ser | Ser | Ala | Lys |
| | | | | | | 130 | | 135 | | 140 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Thr | Pro | Pro | Ser | Val | Tyr | Pro | Leu | Ala | Pro | Gly | Ser | Ala | Ala | Gln |
| | | | | | | 145 | | 150 | | 155 | | 160 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asn | Ser | Met | Val | Thr | Leu | Gly | Cys | Leu | Val | Lys | Gly | Tyr | Phe | Pro |
| | | | | | | 165 | | 170 | | 175 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Pro | Val | Thr | Val | Thr | Trp | Asn | Ser | Gly | Ser | Leu | Ser | Ser | Gly | Val |
| | | | | | | 180 | | 185 | | 190 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser | Asp | Leu | Tyr | Thr | Leu | Ser | Ser |
| | | | | | | 195 | | 200 | | 205 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Thr | Val | Pro | Ser | Ser | Thr | Trp | Pro | Ser | Glu | Thr | Val | Thr | Cys |
| | | | | | | 210 | | 215 | | 220 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Val | Ala | His | Pro | Ala | Ser | Ser | Thr | Lys | Val | Asp | Lys | Lys | Ile | Val |
| | | | | | | 225 | | 230 | | 235 | | 240 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Arg | Asp | Cys | Gly | Cys | Lys | Pro | Cys | Ile | Cys | Thr | Val | Pro | Glu | Val |
| | | | | | | 245 | | 250 | | 255 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Val | Phe | Ile | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Val | Leu | Thr | Ile |
| | | | | | | 260 | | 265 | | 270 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Thr | Pro | Lys | Val | Thr | Cys | Val | Val | Val | Asp | Ile | Ser | Lys | Asp |
| | | | | | | 275 | | 280 | | 285 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Pro | Glu | Val | Gln | Phe | Ser | Trp | Phe | Val | Asp | Asp | Val | Glu | Val | His |
| | | | | | | 290 | | 295 | | 300 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Gln | Thr | Gln | Pro | Arg | Glu | Glu | Gln | Phe | Asn | Ser | Thr | Phe | Arg |
| | | | | | | 305 | | 310 | | 315 | | 320 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Ser | Glu | Leu | Pro | Ile | Met | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

US 9,089,553 B2

139**140**

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| 325 | 330 | 335 | |
|---|-----|-----|-----|
| Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu | | | |
| 340 | 345 | 350 | |
| Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr | | | |
| 355 | 360 | 365 | |
| Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu | | | |
| 370 | 375 | 380 | |
| Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp | | | |
| 385 | 390 | 395 | 400 |
| Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile | | | |
| 405 | 410 | 415 | |
| Met Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln | | | |
| 420 | 425 | 430 | |
| Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His | | | |
| 435 | 440 | 445 | |
| Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro | | | |
| 450 | 455 | 460 | |
| Gly Lys | | | |
| 465 | | | |

<210> SEQ ID NO 140
<211> LENGTH: 1401
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 140

| | | | | | | |
|-------------|-------------|-------------|------------|-------------|------------|------|
| atgggatgga | gctggacatt | tctttcctc | ctgtcaggaa | ctgcaggtgt | cctctctgag | 60 |
| gtccaaactgc | aacagtctgg | acctgaacta | atgaaggctg | gggcttcagt | gaagatgtcc | 120 |
| tgcaaggctt | ctggatatac | attcaactgac | tacaacatgc | actgggtgaa | gcagaaccaa | 180 |
| ggaaagaccc | tagatggat | aggagaaaatt | aatcctaaca | gtgggtggc | tggctacaac | 240 |
| cagaagttca | agggcaaggc | cacattgact | gtagacaagt | cctccaccac | agcctacatg | 300 |
| gagctccgca | gcctgacatc | tgaggactct | gcagtttat | actgtgcaag | attgggctac | 360 |
| gatgatatct | acgacgactg | gtacttcgat | gtctggggcg | cagggaccac | ggtcaccgtc | 420 |
| tcctcagcca | aaacgcacacc | cccatctgtc | tatccactgg | cccctggatc | tgctgccaa | 480 |
| actaactcca | ttgtgaccct | gggatgcctg | gtcaagggct | atttccctga | gccagtgaca | 540 |
| gtgacctgga | actctggatc | cctgtccagc | ggtgtgcaca | cttcccagc | tgtctgcag | 600 |
| tctgacctct | acactctgag | cagtcagtg | actgtcccct | ccagcacctg | gcccagcag | 660 |
| accgtcacct | gcaacgttgc | ccacccggcc | agcagcacca | aggtggacaa | aaaaatttgt | 720 |
| cccaggatt | gtgggtgtaa | gccttgcata | tgtacagtcc | cagaagtatc | atctgtctc | 780 |
| atcttcccc | caaagccaa | ggatgtgctc | accattactc | tgactctaa | ggtcacgtgt | 840 |
| gttgtggtag | acatcagcaa | ggatgatccc | gaggtccagt | tcaagctggtt | tgttagatgt | 900 |
| gtggaggtgc | acacagctca | gacgcaaccc | cgggaggagc | agttcaacag | cactttccgc | 960 |
| taagtcagtg | aactccat | catgcaccag | gactggctca | atggcaagga | gttcaatgc | 1020 |
| agggtcaaca | gtgcagctt | ccctgcccc | atcgagaaaa | ccatctccaa | aaccaaaggc | 1080 |
| agaccgaagg | ctccacaggt | gtacaccatt | ccacctccaa | aggagcagat | ggccaaggat | 1140 |
| aaagtcaagtc | tgacctgcat | gataacagac | ttcttccctg | aagacattac | tgtggagtg | 1200 |
| caagtggaatg | ggcagccagc | ggagaactac | aagaacactc | agcccatcat | ggacacagat | 1260 |

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| | |
|---|------|
| ggcttact tcatctacag caagctcaat gtgcagaaga gcaactggga ggcaggaaat | 1320 |
| acttcacct gctctgtgtt acatgaggc ctgcacaacc accatactga gaagagctc | 1380 |
| tcccaactctc ctggtaatg a | 1401 |

<210> SEQ ID NO 141
<211> LENGTH: 214
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence
<400> SEQUENCE: 141

| | |
|---|--|
| Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly | |
| 1 5 10 15 | |
| Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr | |
| 20 25 30 | |
| Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile | |
| 35 40 45 | |
| Tyr Tyr Thr Ser Arg Leu Leu Ser Gly Val Pro Ser Arg Phe Ser Gly | |
| 50 55 60 | |
| Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro | |
| 65 70 75 80 | |
| Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Thr Leu Pro Tyr | |
| 85 90 95 | |
| Thr Phe Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala | |
| 100 105 110 | |
| Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly | |
| 115 120 125 | |
| Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala | |
| 130 135 140 | |
| Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln | |
| 145 150 155 160 | |
| Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser | |
| 165 170 175 | |
| Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr | |
| 180 185 190 | |
| Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser | |
| 195 200 205 | |
| Phe Asn Arg Gly Glu Cys | |
| 210 | |

<210> SEQ ID NO 142
<211> LENGTH: 642
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody Sequence
<400> SEQUENCE: 142

| | |
|--|-----|
| gacatccaga tgacctcagtc tccatccctcc ctctccgcatt ccgttaggcga ccgcgttaacc | 60 |
| ataaacatgtt gagcatctca agatatttcc aactatttga attggatcca aaaaaaccc | 120 |
| ggcaaaggcac ctaaactcct catttactat acatcaagac tccctccgg cgttccatca | 180 |

-continued

```

cgatttcag gctccggctc cggcacatca ttcacactca ctatccctc cctccaacca      240
gaagatttg caacctatta ctgtcaacaa ggcgatacac tcccatcac ac tccggccgc      300
ggcacaaaag ttgaaattaa acgtacggtg gctgcaccat ctgtcttcat cttccggcca      360
tctgatgac agttgaaatc tggaactgcc tctgttgtgt gctgtgaa taacttctat      420
cccagagagg ccaaagtaca gtggaaaggta gataacgccccc tccaaatcggg taactccag      480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg      540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gctaaatc ccatcaggc       600
ctgagctcgc ccgtcacaaa gagttcaac aggggagagt gt                         642

```

```

<210> SEQ_ID NO 143
<211> LENGTH: 236
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence

```

```
<400> SEQUENCE: 143
```

```

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp
1           5          10          15

```

```

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20          25          30

```

```

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35          40          45

```

```

Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
50          55          60

```

```

Ala Pro Lys Leu Ile Tyr Tyr Ser Arg Leu Leu Ser Gly Val
65          70          75          80

```

```

Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
85          90          95

```

```

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
100         105         110

```

```

Gly Asp Thr Leu Pro Tyr Thr Phe Gly Gly Thr Lys Val Glu Ile
115         120         125

```

```

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130         135         140

```

```

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145         150         155         160

```

```

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
165         170         175

```

```

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180         185         190

```

```

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
195         200         205

```

```

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
210         215         220

```

```

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225         230         235

```

```
<210> SEQ_ID NO 144
```

```
<211> LENGTH: 708
```

```
<212> TYPE: DNA
```

-continued

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 144

```

atggacatga gggccccgc tcagtcctg gggctcctgc tactctggct ccgagggtgcc      60
agatgtgaca tccagatgac ccagtctcca tcctccctct ccgcattccgt aggcgaccgc      120
gttaaccataa catgttagagc atctcaagat atttccaact atttgaattt gtaccaacaa      180
aaaccggca aaggcacctaa actcctcatt tactatacat caagactcct ctccggcggt      240
ccatcacat ttcaggctc cggctccggc acagattca cactcaatat ttccctccctc      300
caaccagaag attttgcac ctattactgt caacaaggcg atacactccc atacacattc      360
ggcgccggca caaaaaggta aattaaacgt acggtggtcg caccatctgt ctcatcttc      420
ccggccatctg atgagcagtt gaaatcttgc actgcctctg ttgtgtgcct gctgaataac      480
ttctatccca gagaggccaa agtacagtgg aaggtggata acggccctcca atcgggtaac      540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cttacagcct cagcagcacc      600
ctgacgctga gcaaaaggaga ctacgagaaa cacaaggct acgcctgcgaa agtcaccat      660
cagggcctga gtcgcccgt cacaaggcgt ttcaacaggc gagagtgt                                708

```

<210> SEQ ID NO 145
<211> LENGTH: 449
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 145

```

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5          10          15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20          25          30

Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35          40          45

Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe
50          55          60

Lys Gly Arg Val Thr Met Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65          70          75          80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85          90          95

Ala Arg Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val
100         105         110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115         120         125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
130         135         140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145         150         155         160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165         170         175

```

-continued

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
195 200 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
210 215 220

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
290 295 300

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> SEQ ID NO 146
<211> LENGTH: 1347
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 146

```

gaggtgcagc tgggtcagag cggcgccgag gtaaaaaaac caggagcaag cgttaaagtt      60
tcttgtaaag caagcgata tacatttaca gattacaaca tgcattgggt aagacaagcg      120
ccaggacaag gattggaatg gatgggcgaa attaaccccta atagtggagg agcaggctac      180
aatcaaaaat tcaaaggag agttacaatg acaacagaca caagcacttc aacagcatat      240
atggaaactgc gatcacttag aagegacgat acagctgtat actattgcgc acgacttggg      300
tatgatgata tatatgatga ctggtatttc gatgtttggg gccaggaaac aacagttacc      360
gtctctagtg cctccaccaa gggcccatcg gtcttcccc tggcgccctg ctccaggagc      420

```

US 9,089,553 B2

149

-continued

150

```

acctccgaga gcacagcggc cctgggctgc ctggtaagg actactccc cgaaccggtg      480
acggtgtcggt ggaactcagg cgctctgacc agcggcgtgc acacccccc agctgtccta      540
cagtcctcag gactctactc cctcagcage gtggtgaccg tgccctccag caacttcggc      600
acccagacct acacctgcaa cgtagatcac aagcccagca acaccaaggt ggacaagaca      660
gtttagcgca aatgttgtgt cgagtgcaca ccgtgcccag caccacctgt ggcaggaccg      720
tcagtcttcc tctttttttt aaaacccaag gacaccctca tgatctcccg gaccctcgag      780
gtcacggtcg tgggtgtgaa cgtgagccac gaagaccccg aggtccagtt caactggtag      840
gtggacggcg tggaggtgca taatgccaag acaaaggccac gggaggagca gttcaacagc      900
acgttccgtg tggtcagcgt cctcaccgtt gtgcaccagg actggctgaa cggcaaggag      960
tacaagtgc aagtctccaa caaaggcctc ccagccccca tcgagaaaaac catctccaaa     1020
accaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggaggagatg     1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct totacccag cgacatcgcc     1140
gtggagtgaa agagcaatgg gcagccggag aacaactaca agaccacacc tcccatgctg     1200
gactccgacg gtccttctt cctctacagc aagtcacccg tggacaagag caggtggcag     1260
caggggaacg tttttcatg ctccgtgatg catgaggotc tgcacaacca ctacacgcag     1320
aagagectct ccctgtctcc gggtaaa                                         1347

```

<210> SEQ ID NO 147

<211> LENGTH: 468

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 147

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Trp | Thr | Trp | Arg | Ile | Leu | Phe | Leu | Val | Ala | Ala | Ala | Thr | Gly |
| 1 | | | | | | 5 | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | His | Ser | Glu | Val | Gln | Leu | Val | Gln | Ser | Gly | Ala | Glu | Val | Lys | Lys |
| | | | | | | 20 | | | 25 | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Ala | Ser | Val | Lys | Val | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe |
| | | | | | | 35 | | | 40 | | | | 45 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asp | Tyr | Asn | Met | His | Trp | Val | Arg | Gln | Ala | Pro | Gly | Gln | Gly | Leu |
| | | | | | | 50 | | | 55 | | | | 60 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Trp | Met | Gly | Glu | Ile | Asn | Pro | Asn | Ser | Gly | Gly | Ala | Gly | Tyr | Asn |
| 65 | | | | | | 70 | | | 75 | | | | 80 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Lys | Phe | Lys | Gly | Arg | Val | Thr | Met | Thr | Thr | Asp | Thr | Ser | Thr | Ser |
| | | | | | | 85 | | | 90 | | | | 95 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Tyr | Met | Glu | Leu | Arg | Ser | Leu | Arg | Ser | Asp | Asp | Thr | Ala | Val |
| | | | | | | 100 | | | 105 | | | | 110 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Cys | Ala | Arg | Leu | Gly | Tyr | Asp | Asp | Ile | Tyr | Asp | Asp | Trp | Tyr |
| 115 | | | | | | 120 | | | 125 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Asp | Val | Trp | Gly | Gln | Gly | Thr | Thr | Val | Thr | Val | Ser | Ser | Ala | Ser |
| 130 | | | | | | 135 | | | 140 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Lys | Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Cys | Ser | Arg | Ser | Thr |
| 145 | | | | | | 150 | | | 155 | | | | 160 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Glu | Ser | Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys | Asp | Tyr | Phe | Pro |
| 165 | | | | | | 170 | | | 175 | | | | | | |

US 9,089,553 B2

151**152**

-continued

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
180 185 190

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
195 200 205

Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr
210 215 220

Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val
225 230 235 240

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
245 250 255

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
260 265 270

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
275 280 285

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
290 295 300

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
305 310 315 320

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
325 330 335

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
340 345 350

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
355 360 365

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
370 375 380

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
405 410 415

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
420 425 430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
435 440 445

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
450 455 460

Ser Pro Gly Lys
465

<210> SEQ ID NO 148

<211> LENGTH: 1404

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 148

```

atggactgga cctggaggat cctttcttg gtggcagcag ccacaggagc ccactccag 60
gtgcagctgg tgcagagcgg cgccgaggta aaaaaaccag gagcaagcgt taaagttct 120
tgtaaagcaa gcggatatac attacagat tacaacatgc attgggtaaag acaagcgcca 180
ggacaaggat tggaatggat gggcgaaatt aaccctaata gtggaggagc aggctacaat 240
caaaaattca aaggggaggt tacaatgaca acagacacaa gcacttcaac agcatatatg 300
gaactgcgt cacttagaag cgacgataca gctgtatact attgcgcacg acttgggtat 360
gatgatataat atgatgactg gtatttcgt gtttggggcc agggaaacaac agttaccgtc 420

```

US 9,089,553 B2

153**154**

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| | | | | | | |
|-------------|------------|-------------|------------|-------------|------------|------|
| tcttagtgcct | ccaccaaggg | cccatcggtc | ttccccctgg | cgcctgctc | caggagcacc | 480 |
| tccgagagca | cagcggccct | gggctgcctg | gtcaaggact | acttccccga | accggtgacg | 540 |
| gtgtcggtga | actcaggcgc | tctgaccagc | ggcgtgcaca | ccttcccagc | tgtcttacag | 600 |
| tcctcaggac | tctactccct | cagcagcgtg | gtgaccgtgc | cctccagcaa | cttcggcacc | 660 |
| cagaccta | cctgcaacgt | agatcacaag | cccagcaaca | ccaagggtga | caagacagt | 720 |
| gagcgcaaat | gttgtgtcga | gtgeccacccg | tgcccgacac | cacctgtggc | aggaccgtca | 780 |
| gtcttcctct | tccccccaaa | acccaaggac | accctcatga | tctccggac | ccctgaggtc | 840 |
| acgtcgctgg | tggtggacgt | gagccacgaa | gaccccgagg | tccagttcaa | ctggtagtgc | 900 |
| gacggcgtgg | aggtgcataa | tgccaagaca | aagccacggg | aggagcagg | caacagcacg | 960 |
| ttccgtgtgg | ttagcgtcct | caccgttg | caccaggact | ggctgaacgg | caaggagtag | 1020 |
| aagtgcagg | tctccaacaa | aggcctccca | gccccatcg | agaaaaccat | ctccaaaacc | 1080 |
| aaagggcagc | cccgagaacc | acagggtgtac | accctgcccc | catccggga | ggagatgacc | 1140 |
| aagaaccagg | ttagcgtgac | ctgcctggtc | aaaggcttct | accccgacgca | catcgccgt | 1200 |
| gagtgggaga | gcaatgggca | gccggagaac | aactacaaga | ccacacctcc | catgtggac | 1260 |
| tccgacggct | ccttcttcct | ctacagcaag | ctcaccgtgg | acaagagcag | gtggcagcag | 1320 |
| gggaacgtct | tctcatgtc | cgtgtatgc | gaggctctgc | acaaccacta | cacgcagaag | 1380 |
| agectctccc | tgtctccggg | taaa | | | | 1404 |

<210> SEQ_ID NO 149

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 149

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Thr | Thr | Ser | Ser | Leu | Ser | Ala | Ser | Leu | Gly |
| 1 | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | 15 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Val | Thr | Ile | Ser | Cys | Arg | Ala | Ser | Gln | Asp | Ile | Ser | Asn | Tyr |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | 30 |
| 20 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Trp | Phe | Gln | Gln | Lys | Pro | Asp | Gly | Thr | Leu | Lys | Leu | Leu | Ile |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | 45 |
| 35 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Tyr | Thr | Ser | Arg | Leu | His | Ser | Gly | Val | Pro | Ser | Arg | Phe | Ser | Gly |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | 60 |
| 50 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Gly | Thr | Asp | Tyr | Ser | Leu | Thr | Ile | Ser | Asn | Leu | Glu | Gln |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | 80 |
| 65 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asp | Ile | Ala | Thr | Tyr | Phe | Cys | Gln | Gln | Gly | Asp | Thr | Leu | Pro | Tyr |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | 95 |
| 85 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Arg | Arg | Ala | Asp | Ala | Ala | |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | 110 |
| 100 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Thr | Val | Ser | Ile | Phe | Pro | Pro | Ser | Ser | Glu | Gln | Leu | Thr | Ser | Gly |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | 125 |
| 115 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ala | Ser | Val | Val | Cys | Phe | Leu | Asn | Asn | Phe | Tyr | Pro | Lys | Asp | Ile |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | 140 |
| 130 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Val | Lys | Trp | Lys | Ile | Asp | Gly | Ser | Glu | Arg | Gln | Asn | Gly | Val | Leu |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | 160 |
| 145 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Trp | Thr | Asp | Gln | Asp | Ser | Lys | Asp | Ser | Thr | Tyr | Ser | Met | Ser |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | 175 |
| 165 | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Leu | Thr | Leu | Thr | Lys | Asp | Glu | Tyr | Glu | Arg | His | Asn | Ser | Tyr |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | 190 |
| 180 | | | | | | | | | | | | | | | |

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser

US 9,089,553 B2

155

-continued

156

 195 200 205

 Phe Asn Arg Asn Glu Cys
 210

<210> SEQ ID NO 150
<211> LENGTH: 645
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 150

| | | |
|---|--------------------------------|-----|
| gatatccaga tgacacagac tacatcctcc | ctgtctgcct ctctggaga cagagtacc | 60 |
| atcagttgc gggcaagtca ggacatttc aatttttaa actggttca gcagaaacca | | 120 |
| gatggaactc ttaaactcct gatcttctac acatcaagat tacactcagg agttccatca | | 180 |
| aggttcagtgc gagtgggtc tggAACAGAT tattcttc aatttttttccatggagccaa | | 240 |
| gaagatatttgc acacttactt ttgccaacag ggtgatacgc ttccgtacac gttcgaaaa | | 300 |
| gggaccaagc tggaaataag acgggctgtat gctgcaccaa ctgtatccat cttccacca | | 360 |
| tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gttcttgc aacttctac | | 420 |
| ccaaaagaca tcaatgtcaa gtggaaagatt gatggcagtg aacgacaaaa tggcgtcctg | | 480 |
| aacagttgga ctgatcagga cagcaaaagac agcacctaca goatgagcag caccctcact | | 540 |
| ttgaccaagg acgagttatga acgacataac agctataccat gtgaggccac tcacaagaca | | 600 |
| tcaacttcac ccattgtcaa gagttcaac aggaatgagt gtttag | | 645 |

<210> SEQ ID NO 151
<211> LENGTH: 234
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 151

| | | | |
|---|-----|-----|-----|
| Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Leu Cys Phe Gln | | | |
| 1 | 5 | 10 | 15 |
| Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser | | | |
| 20 | 25 | 30 | |
| Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp | | | |
| 35 | 40 | 45 | |
| Ile Ser Asn Tyr Leu Asn Trp Phe Gln Gln Lys Pro Asp Gly Thr Leu | | | |
| 50 | 55 | 60 | |
| Lys Leu Leu Ile Phe Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser | | | |
| 65 | 70 | 75 | 80 |
| Arg Phe Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser | | | |
| 85 | 90 | 95 | |
| Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asp | | | |
| 100 | 105 | 110 | |
| Thr Leu Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Arg Arg | | | |
| 115 | 120 | 125 | |
| Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln | | | |
| 130 | 135 | 140 | |
| Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr | | | |
| 145 | 150 | 155 | 160 |
| Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln | | | |
| 165 | 170 | 175 | |
| Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr | | | |
| 180 | 185 | 190 | |

US 9,089,553 B2

157**158**

-continued

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
195 200 205

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
210 215 220

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225 230

<210> SEQ ID NO 152

<211> LENGTH: 705

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 152

| | |
|--|-----|
| atgatgtcct ctgctcagtt ccttggcttc ctgttgcctt gtttcaagg taccagatgt | 60 |
| gatatccaga tgacacagac tacatccctcc ctgtctgcctt ctctgggaga cagagtccacc | 120 |
| atcagttgca gggcaagtca ggacatttgc aattatttaa actggtttca gcagaaacca | 180 |
| gatggaaactc tttaaactcctt gatcttctac acatcaagat tacactcagg agttccatca | 240 |
| aggttcagtg gcagtggttc tggAACAGAT tattctctca ccattagcaa cctggagcaa | 300 |
| gaagatatttgcacttactt ttgccaacag ggtgatacgc ttccgtacac gttcgaaaa | 360 |
| gggaccaagc tggAAATAAG acgggctgtat gctgcaccaa ctgtatccat cttccacca | 420 |
| tccagtgagc agttAACATC tggaggtgcc tcagtcgtgt gtttcttgc aaacttctac | 480 |
| ccccaaagaca tcaatgtcaa gtggaaagatt gatggcagtg aacgacaaaa tggcgtcctg | 540 |
| aacagttgga ctgatcagga cagcaagac agcacctaca gcatgagcag caccctcag | 600 |
| ttgaccaagg acgagttatga acgacataac agctataacct gtgaggccac tcacaagaca | 660 |
| tcaacttcac ccattgtcaa gagttcaac aggaatgagt gttag | 705 |

<210> SEQ ID NO 153

<211> LENGTH: 447

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 153

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Asn Met His Trp Val Lys Gln Asn Gln Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn Pro Asn Ser Gly Gly Ser Gly Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Leu Val Tyr Asp Gly Ser Tyr Glu Asp Trp Tyr Phe Asp Val
100 105 110

Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Pro
115 120 125

Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
130 135 140

Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
145 150 155 160

US 9,089,553 B2

159**160**

-continued

Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe
 165 170 175

 Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
 180 185 190

 Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
 195 200 205

 His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
 210 215 220

 Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val
 225 230 235 240

 Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr
 245 250 255

 Pro Lys Val Thr Cys Val Val Asp Ile Ser Lys Asp Asp Pro Glu
 260 265 270

 Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln
 275 280 285

 Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser
 290 295 300

 Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys
 305 310 315 320

 Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile
 325 330 335

 Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro
 340 345 350

 Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met
 355 360 365

 Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn
 370 375 380

 Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr
 385 390 395 400

 Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn
 405 410 415

 Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu
 420 425 430

 His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 435 440 445

<210> SEQ ID NO 154
 <211> LENGTH: 1344
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 154

```

gagggtccagc tgcaaacagtc tggacctgaa ctaatgaagc ctgggggttc agtgaagatg     60
ttctgcaagg ttctctggata cacattcaact gactacaaca tgcactgggt gaaacagaac   120
caaggaaaga gccttagagtg gataggagaa attaatccta acagtggtgg tagtggctac   180
aaccaaaaagt tcaaaggcaa ggccacattg actgttagaca agtcttccag cacagcctac   240
atggagactcc gcagcctgac atctgaggac tctgcagtc attactgtgc aagattggtc   300
tacgatggca gctacgagga ctggtacttc gatgtctggg ggcgcaggac cacggtcacc   360
gtctcctcag ccaaaaacgac accccccatct gtcttatccac tggccctgg atctgctgcc   420
caaactaact ccatggtgac cctgggatgc ctggtcaagg gctatttccc tgagccagtg   480
acagtgacct ggaactctgg atccctgtcc agcggtgtgc acaccttccc agctgtctg   540

```

```

cagtctgacc tctacactct gagcagctca gtgactgtcc cctccagcac ctggcccagc      600
gagaccgtca cctgcAACGT tgcccACCCG gccagcagca ccaagggtgga caagaaaatt      660
gtgcccaaggg attgtggttg taagccttgc atatgtacag tcccagaagt atcatctgtc      720
ttcatcttcc cccaaAGCC caaggatgtg ctcaccatta ctctgactcc taaggtcacg      780
tgtgttgtagg tagacatcg caaggatgtat cccgagggtcc agttcagctg gttttagat      840
gatgtggagg tgcacacagc tcagacgcaa ccccgggagg agcagttcaa cagcacttc      900
cgctcagtca gtgaacttcc catcatgcac caggactggc tcaatggcaa ggagttcaa      960
tgcagggtca acagtcgcgc ttccctgcc cccatcgaga aaaccatctc caaaaccaa      1020
ggcagaccga aggctccaca ggtgtacacc attccacctc ccaaggagca gatggccaag      1080
gataaaagtca gtctgacctg catgataaca gacttcttcc ctgaagacat tactgtggag      1140
tggcagtggaa atgggcagcc agcggagaac tacaagaaca ctcagccat catggacaca      1200
gatggcttctt acttcatcta cagcaagctc aatgtgcaga agagcaactg ggaggcagga      1260
aataacttca octgctctgt gttacatgag ggctgcaca accaccatac tgagaagagc      1320
ctctccact ctccctggtaa atga                                         1344

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<210> SEQ_ID NO 155
<211> LENGTH: 466
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 155

```

Met Gly Trp Ser Trp Thr Phe Leu Leu Ser Gly Thr Ala Gly
1           5           10          15

Val Leu Ser Glu Val Gln Leu Gln Ser Gly Pro Glu Leu Met Lys
20          25           30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35          40           45

Thr Asp Tyr Asn Met His Trp Val Lys Gln Asn Gln Gly Lys Ser Leu
50          55           60

Glu Trp Ile Gly Glu Ile Asn Pro Asn Ser Gly Gly Ser Gly Tyr Asn
65          70           75           80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
85          90           95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100         105          110

Tyr Tyr Cys Ala Arg Leu Val Tyr Asp Gly Ser Tyr Glu Asp Trp Tyr
115         120          125

Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys
130         135          140

Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln
145         150          155          160

Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro
165         170          175

Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val
180         185          190

His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser
195         200          205

Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys
210         215          220

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Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val
 225 230 235 240

 Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val
 245 250 255

 Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile
 260 265 270

 Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp
 275 280 285

 Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His
 290 295 300

 Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
 305 310 315 320

 Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys
 325 330 335

 Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu
 340 345 350

 Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr
 355 360 365

 Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu
 370 375 380

 Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp
 385 390 395 400

 Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile
 405 410 415

 Met Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln
 420 425 430

 Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His
 435 440 445

 Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro
 450 455 460

 Gly Lys
 465

<210> SEQ ID NO 156

<211> LENGTH: 1401

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 156

```

atgggatgga gctggacctt tctttcctc ctgtcaggaa ctgcaggtgt cctctctgag        60
gtccagctgc aacagtctgg acctgaacta atgaagcctg gggcttcagt gaagatgtcc    120
tgcaaggctt ctggatacac attcaactgac tacaacatgc actgggtgaa acagaaccaa    180
ggaaagagcc tagagtggat aggagaaatt aatcctaaca gtgggtggtag tggctacaac    240
caaaagttca aaggcaaggc cacattgact gtagacaagt cttccagcac agcctacatg    300
gagctccgca gcctgacatc tgaggactct gcagtctatt actgtgcaag attggctac    360
gatggcagct acgaggactg gtacttcgat gtctggggcg cagggaccac ggtcaccgtc    420
tcctcagcca aaacgacacc cccatctgtc tatccactgg cccctggatc tgctgccaa    480
actaactcca tggtgaccct gggatgcctg gtcaaggcgt atttccctga gccagtgaca    540
gtgacctgga actctggatc cctgtccagc ggtgtgcaca cttcccagc tgtctgcag    600
tctgacacct acactctgag cagctcagtg actgtccccct ccagcacctg gcccagcgag    660
accgtcacct gcaacgttgc ccacccggcc agcagcacca aggtggacaa gaaaatttgt    720

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```

cccagggatt gtggttgtaa gccttgcata tgtacagtcc cagaagtatc atctgtctc    780
atcttcccccaaaagccaa ggtatgtgctc accattactc tgactcctaa ggtcacgtgt    840
gttgtggtag acatcagcaa ggatgatccc gaggtccagt tcaagctggtt tgttagatgat    900
gtggagggtgc acacagctca gacgcacacc cgggaggagc agttcaacag cacttccgc    960
tcagtcagtg aacttcccat catgcaccag gactggctca atggcaagga gttcaaatgc   1020
agggtcaaca gtgcagctt ccctgcccc atcgagaaaa ccatctccaa aaccaaaggc   1080
agaccgaagg ctccacaggt gtacaccatt ccacctccaa aggagcagat ggccaaggat   1140
aaagtcaagtc tgacctgcatt gataacagac ttcttcctg aagacattac tggggagtgg   1200
cagtggaatg ggcagccagc ggagaactac aagaacactc agcccatcat ggacacagat   1260
ggctcttaact tcatactacag caagtcataa gtgcagaaga gcaactggga ggcaggaaat   1320
actttcacct gctctgtgtt acatgagggc ctgcacaacc accataactga gaagagcctc   1380
tcccaacttc ctggtaatg a                                         1401

```

<210> SEQ ID NO 157

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 157

```

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1           5           10          15

Asp Arg Val Thr Ile Cys Cys Arg Ala Ser Gln Val Ile Thr Asn Tyr
20          25           30

Leu Tyr Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe Lys Leu Leu Ile
35          40           45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50          55           60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65          70           75           80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
85          90           95

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala
100         105          110

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
115         120          125

Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
130         135          140

Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
145         150          155          160

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
165         170          175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
180         185          190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
195         200          205

Phe Asn Arg Asn Glu Cys
210

```

<210> SEQ ID NO 158

<211> LENGTH: 642

<212> TYPE: DNA

-continued

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 158

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|------------|-----|
| gataccaga | tgacacagac | tacatccctc | ctgtctgc | ctctggaga | cagagtacc | 60 |
| atctgttca | ggcaagtca | ggtcattacc | aattatttat | actggtatca | gcagaaacca | 120 |
| gatggactt | ttaaactcct | gatctactac | acatcaagat | tacactcagg | agtcccac | 180 |
| aggttcagt | gcagtgggtc | tggacacat | tattctctca | ccattagcaa | cctggAACAG | 240 |
| gaagatattt | ccacttactt | ttgccaacag | ggtgatacgc | ttccgtacac | gttcggaggg | 300 |
| gggaccaagc | tggaaataaa | acgggctgtat | gctgcaccaa | ctgtatccat | cttcccacca | 360 |
| tccagtgagc | agttAACATC | tggaggtgcc | tcagtcgtgt | gtttcttggaa | caacttctac | 420 |
| cccaaaagaca | tcaatgtcaa | gtggaaagatt | gatggcagt | aacgacaaaa | tggcgtctg | 480 |
| aacagtttga | ctgatcagga | cagcaaagac | agcacctaca | gcatgagcag | caccctcact | 540 |
| ttgaccaagg | acgagttatga | acgacataac | agctataacct | gtgaggccac | tcacaagaca | 600 |
| tcaacttcac | ccattgtcaa | gagcttcaac | aggaatgagt | gt | | 642 |

<210> SEQ ID NO 159

<211> LENGTH: 234

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 159

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Ser | Ser | Ala | Gln | Phe | Leu | Gly | Leu | Leu | Leu | Cys | Phe | Gln |
| 1 | | | | 5 | | | 10 | | 15 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Thr | Arg | Cys | Asp | Ile | Gln | Met | Thr | Gln | Thr | Thr | Ser | Ser | Leu | Ser |
| | | | | | 20 | | | 25 | | 30 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Leu | Gly | Asp | Arg | Val | Thr | Ile | Cys | Cys | Arg | Ala | Ser | Gln | Val |
| | | | | | 35 | | | 40 | | 45 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Thr | Asn | Tyr | Leu | Tyr | Trp | Tyr | Gln | Gln | Lys | Pro | Asp | Gly | Thr | Phe |
| | | | | | 50 | | | 55 | | 60 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Leu | Leu | Ile | Tyr | Tyr | Thr | Ser | Arg | Leu | His | Ser | Gly | Val | Pro | Ser |
| | | | | | 65 | | | 70 | | 75 | | 80 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Arg | Phe | Ser | Gly | Ser | Gly | Thr | Asp | Tyr | Ser | Leu | Thr | Ile | Ser | | |
| | | | | | 85 | | | 90 | | 95 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Leu | Glu | Gln | Glu | Asp | Ile | Ala | Thr | Tyr | Phe | Cys | Gln | Gly | Asp | |
| | | | | | 100 | | | 105 | | 110 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Leu | Pro | Tyr | Thr | Phe | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg | |
| | | | | | 115 | | | 120 | | 125 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asp | Ala | Ala | Pro | Thr | Val | Ser | Ile | Phe | Pro | Pro | Ser | Ser | Glu | Gln |
| | | | | | 130 | | | 135 | | 140 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Thr | Ser | Gly | Gly | Ala | Ser | Val | Val | Cys | Phe | Leu | Asn | Asn | Phe | Tyr |
| | | | | | 145 | | | 150 | | 155 | | 160 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Lys | Asp | Ile | Asn | Val | Lys | Trp | Lys | Ile | Asp | Gly | Ser | Glu | Arg | Gln |
| | | | | | 165 | | | 170 | | 175 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Gly | Val | Leu | Asn | Ser | Trp | Thr | Asp | Gln | Asp | Ser | Lys | Asp | Ser | Thr |
| | | | | | 180 | | | 185 | | 190 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ser | Met | Ser | Ser | Thr | Leu | Thr | Leu | Thr | Lys | Asp | Glu | Tyr | Glu | Arg |
| | | | | | 195 | | | 200 | | 205 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Asn | Ser | Tyr | Thr | Cys | Glu | Ala | Thr | His | Lys | Thr | Ser | Thr | Ser | Pro |
| | | | | | 210 | | | 215 | | 220 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|
| Ile | Val | Lys | Ser | Phe | Asn | Arg | Asn | Glu | Cys | | | | | | |
| | | | | | 225 | | | 230 | | | | | | | |

US 9,089,553 B2

169

-continued

<210> SEQ ID NO 160
<211> LENGTH: 702
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 160

```
atgatgtcct ctgctcagtt ccttggcttc ctgttgcctt gtttcaagg taccagatgt      60
gataccaga tgacacagac tacatccctcc ctgtctgcctt ctctgggaga cagagtccacc    120
atctgttgca gggcaagtca ggtcattacc aattatttat actggatcatca gcagaaacca    180
gatggaaacctt tttaactcctt gatctactac acatcaagat tacactcagg agtccccatca  240
aggttcagtg gcagtgggtc tggAACAGAT tattctctca ccattagcaa cctggAACAG    300
gaagatatttccacttactt ttgccaacag ggtgatacgc ttccgtacac gttcgagggg    360
gggaccaagc tggAAATAAA acgggctgat gctgcaccaa ctgtatccat cttccacca    420
tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gtttcttgc aaacttctac    480
cccaaagaca tcaatgtcaa tggAAAGATT gatggcagtg aacgacaaaa tggcgtcctg    540
aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg    600
ttgaccaagg acgagttatga acgacataac agctataacct gtgaggccac tcacaagaca  660
tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gt                         702
```

<210> SEQ ID NO 161
<211> LENGTH: 447
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 161

```
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly Ala
1           5          10          15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20          25          30
Asn Met His Trp Met Lys Gln Asn Gln Gly Lys Ser Leu Glu Trp Ile
35          40          45
Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Gln Phe
50          55          60
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Arg Thr Ala Tyr
65          70          75          80
Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85          90          95
Ala Arg Leu Gly Tyr Val Gly Asn Tyr Glu Asp Trp Tyr Phe Asp Val
100         105         110
Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Pro
115         120         125
Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
130         135         140
Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
145         150         155         160
Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe
165         170         175
Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
180         185         190
Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
195         200         205
```

170

-continued

His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
 210 215 220
 Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val
 225 230 235 240
 Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr
 245 250 255
 Pro Lys Val Thr Cys Val Val Asp Ile Ser Lys Asp Asp Pro Glu
 260 265 270
 Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln
 275 280 285
 Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser
 290 295 300
 Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys
 305 310 315 320
 Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro
 340 345 350
 Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met
 355 360 365
 Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn
 370 375 380
 Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr
 385 390 395 400
 Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn
 405 410 415
 Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu
 420 425 430
 His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 435 440 445

<210> SEQ ID NO 162
 <211> LENGTH: 1341
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 162

```

gagggtccagc tgcaacagtc tggacctgaa ctaatgaagc ctggggcttc agtgaagatg      60
tcctgcaggc cttctggata cacattcaact gactacaaca tgcactggat gaagcagaac      120
caaggaaaaga gcctagaatg gataggagaa attaatccta acagtgggtgg tgctggctac      180
aaccagcagt tcaaaggcaa ggccacattt actgttagaca agtcctccag gacagcctac      240
atggagactcc gcagcctgac atctgaggac tctgcagtctt attactgtgc aagattggc      300
tacgttggta attacgagga ctggtacttc gatgtctggg ggcgcaggagcac cacggtcacc      360
gtctcctcag ccaaaacgac accccccatct gtcttatccac tggccctgg atctgtgcc      420
caaactaact ccatggtgac cctgggatgc ctggtaagg gctatttccc tgagccagt      480
acagtgcacct ggaactctgg atccctgtcc agcgggtgtgc acaccttccc agctgtctg      540
cagtcgtgacc tctacactct gagcagctca gtgactgtcc cttccagcac ctggcccagc      600
gagaccgtca cctgcaacgt tgcccacccg gccagcagca ccaaggtgga caagaaaatt      660
gtgcccaggg attgtggttt taagccttgc atatgtacag tcccagaagt atcatctgtc      720
ttcatcttcc cccaaagcc caaggatgtc ctcaccatta ctctgactcc taaggtcacf      780

```

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| | | | | | | |
|-------------|------------|---------------|-------------|------------|-------------|------|
| tgtgttgtgg | tagacatcg | caaggatgtatcc | cccgagggtcc | agttcagctg | gtttgttagat | 840 |
| gatgtggagg | tgcacacagc | tcagacgcaa | ccccggggagg | agcagttcaa | cagcacttc | 900 |
| cgctcagtca | gtgaacttcc | catcatgcac | caggactggc | tcaatggcaa | ggagttcaaa | 960 |
| tgcagggtca | acagtgccgc | tttccctgcc | cccatcgaga | aaaccatctc | caaaacccaaa | 1020 |
| ggcagaccga | aggctccaca | ggtgtcacacc | attccaccc | ccaaggagca | gatggccaaag | 1080 |
| gataaaagtca | gtctgacctg | catgataaca | gacttcttcc | ctgaagacat | tactgtggag | 1140 |
| tggcagtggaa | atgggcagcc | agcggagaac | tacaagaaca | ctcagccat | catggacaca | 1200 |
| gatggctctt | acttcatcta | cagcaagctc | aatgtgcaga | agagcaactg | ggaggccagga | 1260 |
| aataacttca | cctgtctgt | gttacatgag | ggcctgcaca | accaccatac | tgagaagagc | 1320 |
| ctctcccaact | ctcctggtaa | a | | | | 1341 |

<210> SEQ_ID NO 163

<211> LENGTH: 466

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 163

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Trp | Ser | Trp | Thr | Phe | Leu | Phe | Leu | Leu | Ser | Gly | Thr | Ala | Gly |
| 1 | | | | | | | | | | | | | | | 15 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ser | Glu | Val | Gln | Leu | Gln | Ser | Gly | Pro | Glu | Leu | Met | Lys |
| | | | | 20 | | | | 25 | | | | | 30 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Ala | Ser | Val | Lys | Met | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe |
| | | | | | | 35 | | 40 | | | | | 45 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asp | Tyr | Asn | Met | His | Trp | Met | Lys | Gln | Asn | Gln | Gly | Lys | Ser | Leu |
| | | | | | | 50 | | 55 | | | | | 60 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Trp | Ile | Gly | Glu | Ile | Asn | Pro | Asn | Ser | Gly | Gly | Ala | Gly | Tyr | Asn |
| | | | | | | 65 | | 70 | | | | | 80 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Gln | Phe | Lys | Gly | Lys | Ala | Thr | Leu | Thr | Val | Asp | Lys | Ser | Ser | Arg |
| | | | | | | 85 | | 90 | | | | | 95 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Tyr | Met | Glu | Leu | Arg | Ser | Leu | Thr | Ser | Glu | Asp | Ser | Ala | Val |
| | | | | | | 100 | | 105 | | | | | 110 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Cys | Ala | Arg | Leu | Gly | Tyr | Val | Gly | Asn | Tyr | Glu | Asp | Trp | Tyr |
| | | | | | | 115 | | 120 | | | | | 125 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Asp | Val | Trp | Gly | Ala | Gly | Thr | Thr | Val | Thr | Val | Ser | Ser | Ala | Lys |
| | | | | | | 130 | | 135 | | | | | 140 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Thr | Pro | Pro | Ser | Val | Tyr | Pro | Leu | Ala | Pro | Gly | Ser | Ala | Ala | Gln |
| | | | | | | 145 | | 150 | | | | | 160 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asn | Ser | Met | Val | Thr | Leu | Gly | Cys | Leu | Val | Lys | Gly | Tyr | Phe | Pro |
| | | | | | | 165 | | 170 | | | | | 175 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Pro | Val | Thr | Val | Thr | Trp | Asn | Ser | Gly | Ser | Leu | Ser | Ser | Gly | Val |
| | | | | | | 180 | | 185 | | | | | 190 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser | Asp | Leu | Tyr | Thr | Leu | Ser | Ser |
| | | | | | | 195 | | 200 | | | | | 205 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Thr | Val | Pro | Ser | Ser | Thr | Trp | Pro | Ser | Glu | Thr | Val | Thr | Cys |
| | | | | | | 210 | | 215 | | | | | 220 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Val | Ala | His | Pro | Ala | Ser | Ser | Thr | Lys | Val | Asp | Lys | Lys | Ile | Val |
| | | | | | | 225 | | 230 | | | | | 240 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Arg | Asp | Cys | Gly | Cys | Lys | Pro | Cys | Ile | Cys | Thr | Val | Pro | Glu | Val |
| | | | | | | 245 | | 250 | | | | | 255 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Val | Phe | Ile | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Val | Leu | Thr | Ile |
| | | | | | | 260 | | 265 | | | | | 270 | | |

-continued

Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp
 275 280 285
 Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His
 290 295 300
 Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
 305 310 315 320
 Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys
 325 330 335
 Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu
 340 345 350
 Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr
 355 360 365
 Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu
 370 375 380
 Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp
 385 390 395 400
 Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile
 405 410 415
 Met Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln
 420 425 430
 Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His
 435 440 445
 Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro
 450 455 460
 Gly Lys
 465

<210> SEQ ID NO 164
 <211> LENGTH: 1398
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 164

```

atgggatgga gctggacctt tctttcctc ctgtcaggaa ctgcaggtgt cctctctgag      60
gtccagctgc aacagtctgg acctgaacta atgaagcctg gggcttcagt gaagatgtcc     120
tgcaaggctt ctggatacac attcaactgac tacaacatgc actggatgaa gcagaaccaa     180
ggaaagagcc tagaatggat aggagaaatt aatcctaaca gtgggttgtc tggctacaac     240
cagcagttca aaggcaaggc cacattgact qtagacaagt cttccaggac agcctacatg     300
gagctccgca gcctgacatc tgaggactct gcagtctatt actgtgcaag attgggctac     360
gttggtaatt acgaggactg gtacttcgat gtctgggatc cagggaccac ggtcaccgtc     420
tcctcagcca aaacgacacc cccatctgtc tatccactgg cccctggatc tgctgccaa     480
actaactcca tggtgacctt gggatgcctg gtcaagggtt atttccctga gccagtgaca     540
gtgacctgga actctggatc cctgtccagc ggtgtgcaca cttcccagc tgtcctgcag     600
tctgacacctt acactctgag cagctcagtg actgtccccct ccagcacctg gcccagcgag     660
accgtcacct gcaacgttgc ccacccggcc agcagcacca aggtggacaa gaaaatttg      720
cccaggatt gtgggtgtaa gcctgcata tgcacagtcc cagaagtatc atctgtctc     780
atcttccccca caaagccaa ggatgtgtc accattactc tgactcctaa ggtcacgtgt     840
gttgggttag acatcagcaa ggatgatccc gaggtccagt tcagctggtt tgttagatgat     900
gtggaggtgc acacagctca gacgcaaccc cgggaggagc agttcaacag cactttccgc     960
  
```

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| | | | | | | | | | | | | | | |
|------|------|------|-----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------|
| tca | gtc | agtg | aacttccat | catgcaccag | gactggctca | atggcaagga | gttcaaatgc | 1020 | | | | | | |
| agg | gtc | aaca | gtc | cac | cccc | atcgagaaaa | ccatctccaa | aaccaaaggc | 1080 | | | | | |
| agac | ccg | aagg | ctcc | acaggt | gtacaccatt | ccac | ctccca | aggagcagat | ggccaaggat | 1140 | | | | |
| aaag | tgc | tcag | tc | tgac | ctgc | atgc | aac | acagac | ttcttccctg | aagacattac | tgtggagtgg | 1200 | | |
| cagt | gga | atg | ggc | agcc | cage | ggaga | actac | aaga | acactc | agccc | atcat | ggacacagat | 1260 | |
| ggct | tct | ta | ct | tc | atct | acag | caag | tc | actgg | gaga | gttgc | ggcaggaaat | 1320 | |
| actt | tcac | ct | ct | gt | ctgt | gtt | acat | gagg | gc | caca | acc | atactg | gaagagctc | 1380 |
| tccc | act | c | tctc | ct | ggtaaa | | | | | | | | | 1398 |

<210> SEQ ID NO 165

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 165

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Thr | Thr | Ser | Ser | Leu | Ser | Ala | Ser | Leu | Gly |
| 1 | | | | | 5 | | | 10 | | | 15 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Val | Ser | Ile | Ser | Cys | Arg | Ala | Ser | Gln | Asp | Ile | Ser | Asn | Tyr |
| | | | | 20 | | | | 25 | | | | 30 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Trp | Tyr | Gln | Gln | Lys | Pro | Asp | Gly | Thr | Phe | Lys | Leu | Leu | Ile |
| | | | | 35 | | 40 | | | | 45 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Tyr | Thr | Ser | Arg | Leu | Leu | Ser | Gly | Val | Pro | Ser | Arg | Phe | Ser | Gly |
| | | | | 50 | | | 55 | | | 60 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Gly | Thr | Asp | Tyr | Ser | Leu | Thr | Ile | Tyr | Asn | Leu | Glu | Gln |
| | | | | 65 | | | 70 | | 75 | | 80 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asp | Phe | Ala | Thr | Tyr | Phe | Cys | Gln | Gln | Gly | Asp | Thr | Leu | Pro | Tyr |
| | | | | 85 | | | 90 | | | | 95 | | | | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg | Ala | Asp | Ala | Ala |
| | | | | 100 | | 105 | | | 110 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Thr | Val | Ser | Ile | Phe | Pro | Pro | Ser | Ser | Glu | Gln | Leu | Thr | Ser | Gly |
| | | | | 115 | | 120 | | 125 | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ala | Ser | Val | Val | Cys | Phe | Leu | Asn | Asn | Phe | Tyr | Pro | Lys | Asp | Ile |
| | | | | 130 | | 135 | | 140 | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Val | Lys | Trp | Lys | Ile | Asp | Gly | Ser | Glu | Arg | Gln | Asn | Gly | Val | Leu |
| 145 | | | | 150 | | | 155 | | | 160 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Trp | Thr | Asp | Gln | Asp | Ser | Lys | Asp | Ser | Thr | Tyr | Ser | Met | Ser |
| | | | | 165 | | | 170 | | | 175 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Leu | Thr | Leu | Thr | Lys | Asp | Glu | Tyr | Glu | Arg | His | Asn | Ser | Tyr |
| | | | | 180 | | 185 | | | 190 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Cys | Glu | Ala | Thr | His | Lys | Thr | Ser | Thr | Ser | Pro | Ile | Val | Lys | Ser |
| | | | | 195 | | 200 | | 205 | | | | | | | |

| | | | | | |
|-----|-----|-----|-----|-----|-----|
| Phe | Asn | Arg | Asn | Glu | Cys |
| | | | | 210 | |

<210> SEQ ID NO 166

<211> LENGTH: 645

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 166

| | | | | | | | | | | | | | | | | | | | |
|-----|------|-----|------|------|----|----|-----|---|---|----|----|----|----|---|-----|----|----|----|----|
| gat | atcc | aga | tgac | acag | ac | ta | cat | c | c | ct | gt | tc | gc | c | agg | gt | tc | cc | 60 |
|-----|------|-----|------|------|----|----|-----|---|---|----|----|----|----|---|-----|----|----|----|----|

| | | | | | | | | | | | | | | | | | | | |
|-----|------|-----|-----|----|----|----|----|------|----|----|----|----|----|----|----|----|----|----|-----|
| atc | agtt | gca | ggc | aa | gt | ca | ag | catt | ag | ca | tt | tt | tc | ta | tt | tc | tt | tc | 120 |
|-----|------|-----|-----|----|----|----|----|------|----|----|----|----|----|----|----|----|----|----|-----|

| | | | | | | | | | | | | | | | | | | | |
|-----|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|
| gat | g | ga | ac | tt | ct | ta | tt | tc | ac | at | ca | aa | gt | tc | cc | at | ca | tt | 180 |
|-----|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|

```

aggttcagtgcagtggtc tggAACAGAT tattctctca ccatttacaa cctggagcaa 240
gaagatTTGccAAACAG ggagatacgc ttccgtacac tttcgagg 300
gggaccAAAC tggAAATAAA acgggctgat gctgcaccaa ctgtatccat cttcccacca 360
tccagtGAGC agttaacatc tggaggtgcc tcagtcgtgt gtttcttGAA caacttctac 420
cccaaaAgaca tcaatgtcaa gtggaaagatt gatggcagtg aacgacaaa tggcgtcctg 480
aacagtTGGG ctgatcagga cagcaaAGAC agcacctaca gcatgagcag caccctcACG 540
ttgaccaagg acgagtatGA acgacataac agtataacct gtgaggccac tcacaagaca 600
tcaacttcac ccattgtcaa gagttcaac aggaatgagt gttag 645

```

<210> SEQ ID NO 167

<211> LENGTH: 234

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 167

```

Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Cys Phe Gln
1 5 10 15
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser
20 25 30
Ala Ser Leu Gly Asp Arg Val Ser Ile Ser Cys Arg Ala Ser Gln Asp
35 40 45
Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe
50 55 60
Lys Leu Leu Ile Phe Tyr Thr Ser Arg Leu Leu Ser Gly Val Pro Ser
65 70 75 80
Arg Phe Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Tyr
85 90 95
Asn Leu Glu Gln Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asp
100 105 110
Thr Leu Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125
Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
130 135 140
Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
145 150 155 160
Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
165 170 175
Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
180 185 190
Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
195 200 205
His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
210 215 220
Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225 230

```

<210> SEQ ID NO 168

<211> LENGTH: 705

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 168

```

atgatgtcct ctgctcagtt ccttggctc ctgttgcctt gtttcaagg taccagatgt 60

```

-continued

gatatccaga tgacacagac tacatcctcc ctgtctgcct ctctggaga cagggtctcc 120
 atcagttgca gggcaagtca agacatttc aatttattaa actggtatca gcagaaacca 180
 gatggaaacct ttaaactcct tatcttctac acatcaagat tactctcagg agtcccacca 240
 aggttcagtg gcagtggtc tgaaacagat tattctctca ccatttacaa cctggagcaa 300
 gaagattttg ccacttactt ttgccaacag ggagatacgc ttccgtacac tttcgagg 360
 gggaccaaac tggaaataaa acgggctgtat gctgcaccaa ctgtatccat cttccacca 420
 tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gtttttgaa caacttctac 480
 cccaaagaca tcaatgtcaa gtggaagatt gatggcagt aacgacaaa tggcgtcctg 540
 aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg 600
 ttgaccaagg acgagttatga acgacataac agtatacct gtgaggccac tcacaagaca 660
 tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gttag 705

<210> SEQ ID NO 169

<211> LENGTH: 447

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 169

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Gln | Gln | Ser | Gly | Pro | Glu | Leu | Met | Lys | Pro | Gly | Ala |
| 1 | | | | | | | | | 5 | | 10 | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Lys | Met | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe | Thr | Asp | Tyr |
| | | | | | | | | | 20 | | 25 | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Met | His | Trp | Val | Lys | Gln | Asn | Gln | Gly | Lys | Thr | Leu | Asp | Trp | Ile |
| | | | | | | | | | 35 | | 40 | | 45 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Glu | Ile | Asn | Pro | Asn | Ser | Gly | Gly | Ala | Gly | Tyr | Asn | Gln | Lys | Phe |
| | | | | | | | | 50 | | 55 | | 60 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gly | Lys | Ala | Thr | Leu | Thr | Val | Asp | Lys | Ser | Ser | Thr | Thr | Ala | Tyr |
| 65 | | | | | | | | 70 | | 75 | | 80 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Arg | Ser | Leu | Thr | Ser | Glu | Asp | Ser | Ala | Val | Tyr | Tyr | Cys |
| | | | | | | | | 85 | | 90 | | 95 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Arg | Leu | Gly | Tyr | Asp | Asp | Ile | Tyr | Asp | Asp | Trp | Tyr | Phe | Asp | Val |
| | | | | | | | 100 | | 105 | | 110 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Gly | Ala | Gly | Thr | Thr | Val | Thr | Val | Ser | Ser | Ala | Lys | Thr | Thr | Pro |
| | | | | | | | 115 | | 120 | | 125 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Val | Tyr | Pro | Leu | Ala | Pro | Gly | Ser | Ala | Ala | Gln | Thr | Asn | Ser |
| | | | | | | | 130 | | 135 | | 140 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Thr | Leu | Gly | Cys | Leu | Val | Lys | Gly | Tyr | Phe | Pro | Glu | Pro | Val |
| 145 | | | | | | | | 150 | | 155 | | 160 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Val | Thr | Trp | Asn | Ser | Gly | Ser | Leu | Ser | Ser | Gly | Val | His | Thr | Phe |
| | | | | | | | 165 | | 170 | | 175 | | | | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | Val | Leu | Gln | Ser | Asp | Leu | Tyr | Thr | Leu | Ser | Ser | Val | Thr |
| | | | | | | | 180 | | 185 | | 190 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Ser | Ser | Thr | Trp | Pro | Ser | Glu | Thr | Val | Thr | Cys | Asn | Val | Ala |
| | | | | | | | 195 | | 200 | | 205 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Pro | Ala | Ser | Ser | Thr | Lys | Val | Asp | Lys | Lys | Ile | Val | Pro | Arg | Asp |
| | | | | | | 210 | | 215 | | 220 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Gly | Cys | Lys | Pro | Cys | Ile | Cys | Thr | Val | Pro | Glu | Val | Ser | Ser | Val |
| 225 | | | | | | | | 230 | | 235 | | 240 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ile | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Val | Leu | Thr | Ile | Thr | Leu | Thr |
| | | | | | | | 245 | | 250 | | 255 | | | | |

-continued

Pro Lys Val Thr Cys Val Val Asp Ile Ser Lys Asp Asp Pro Glu
260 265 270

Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln
275 280 285

Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser
290 295 300

Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys
305 310 315 320

Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile
325 330 335

Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro
340 345 350

Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met
355 360 365

Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn
370 375 380

Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr
385 390 395 400

Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn
405 410 415

Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu
420 425 430

His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
435 440 445

<210> SEQ_ID NO 170

<211> LENGTH: 1344

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 170

gaggtccaac tgcaacagtc tggacctgaa ctaatgaagc ctggggcttc agtgaagatg 60
 tcctgcaagg cttctggata tacattcaact gactacaaca tgcactgggt gaagcagaac 120
 caaggaaaga cccttagactg gataggagaa attaatccta acagtgggtgg tgctggctac 180
 aaccagaagt tcaaggggcaa ggccacattg actgttagaca agtcctccac cacagcctac 240
 atggagctcc gcagectgac atctgaggac tctgcagtctt attactgtgc aagattgggc 300
 tacgatgata tctacgacga ctggtacttc gatgtctggg ggcgcaggac cacggtcacc 360
 gtctcctcg ccaaaaacgac accccccatct gtcttatccac tggcccttg atctgctgcc 420
 caaactaact ccatggtgac cctgggatgc ctggtaagg gctatttccc tgagccagtg 480
 acagtgcacctt ggaactctgg atccctgtcc agcgggtgtgc acaccttccc agctgtcctg 540
 cagtctgacc tctacactct gagcagctca gtgactgtcc cctccagcac ctggcccagc 600
 gagaccgtca octgcaacgt tgcccaccccg gccagcgcac ccaagggtgga caagaaaatt 660
 gtgcccaggg atttgtggttg taagccttgc atatgtacag tcccagaagt atcatctgtc 720
 ttcatcttcc ccccaaagcc caaggatgtg ctcaccatca ctctgactcc taaggtcact 780
 tgtgttgtgg tagacatcag caaggatgtat cccgagggtcc agttcagctg gtttgttagat 840
 gatgtggagg tgcacacagc tcagacgcaa ccccgaggagg agcagttcaa cagcacttc 900
 cgctcagtcgtca gtgaacttcc catcatgcac caggactggc tcaatggcaa ggagtcaaa 960
 tgcagggtca acagtgcagc ttccctgccc cccatcgaga aaaccatctc caaaaccaaa 1020
 ggcagaccga aggctccaca ggtgtacacc attccacctc ccaaggagca gatggccaag 1080

-continued

```

gataaaagtca gtctgacctg catgataaca gacttcttcc ctgaagacat tactgtggag    1140
tggcagtggaa atgggcagcc agcggagaac tacaagaaca ctcagccat catggacaca    1200
gatggctttt acttcatcta cagcaagctc aatgtgcaga agagcaactg ggaggcagga    1260
aataactttca cctgtctgtt gttacatgag ggcctgcaca accaccatac tgagaagagc    1320
ctctcccact tcctcgtaa atga                                         1344

```

<210> SEQ ID NO 171

<211> LENGTH: 466

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 171

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Trp | Ser | Trp | Thr | Phe | Leu | Phe | Leu | Ser | Gly | Thr | Ala | Gly |
| 1 | | | | | | | | | | | | | | |
| | | | | | | | 5 | | 10 | | | 15 | | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ser | Glu | Val | Gln | Leu | Gln | Ser | Gly | Pro | Glu | Leu | Met | Lys |
| | | | | | | | | | | | | | | |
| | | | | 20 | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Ala | Ser | Val | Lys | Met | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe |
| | | | | | | | | | | | | | | | |
| | | | | | | 35 | 40 | | | | 45 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asp | Tyr | Asn | Met | His | Trp | Val | Lys | Gln | Asn | Gln | Gly | Lys | Thr | Leu |
| | | | | | | | | | | | | | | | |
| | | | | | | 50 | 55 | | | | 60 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Trp | Ile | Gly | Glu | Ile | Asn | Pro | Asn | Ser | Gly | Gly | Ala | Gly | Tyr | Asn |
| | | | | | | | | | | | | | | | |
| | | | | | | 65 | 70 | | | 75 | | 80 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Lys | Phe | Lys | Gly | Lys | Ala | Thr | Leu | Thr | Val | Asp | Lys | Ser | Ser | Thr |
| | | | | | | | | | | | | | | | |
| | | | | | | 85 | 90 | | | 95 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Tyr | Met | Glu | Leu | Arg | Ser | Leu | Thr | Ser | Glu | Asp | Ser | Ala | Val |
| | | | | | | | | | | | | | | | |
| | | | | | | 100 | 105 | | | 110 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Cys | Ala | Arg | Leu | Gly | Tyr | Asp | Asp | Ile | Tyr | Asp | Asp | Trp | Tyr |
| | | | | | | | | | | | | | | | |
| | | | | | | 115 | 120 | | | 125 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Asp | Val | Trp | Gly | Ala | Gly | Thr | Thr | Val | Thr | Val | Ser | Ser | Ala | Lys |
| | | | | | | | | | | | | | | | |
| | | | | | | 130 | 135 | | | 140 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Thr | Pro | Pro | Ser | Val | Tyr | Pro | Leu | Ala | Pro | Gly | Ser | Ala | Ala | Gln |
| | | | | | | | | | | | | | | | |
| | | | | | | 145 | 150 | | 155 | | 160 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asn | Ser | Met | Val | Thr | Leu | Gly | Cys | Leu | Val | Lys | Gly | Tyr | Phe | Pro |
| | | | | | | | | | | | | | | | |
| | | | | | | 165 | 170 | | | 175 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Pro | Val | Thr | Val | Thr | Trp | Asn | Ser | Gly | Ser | Leu | Ser | Ser | Gly | Val |
| | | | | | | | | | | | | | | | |
| | | | | | | 180 | 185 | | | 190 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser | Asp | Leu | Tyr | Thr | Leu | Ser | Ser |
| | | | | | | | | | | | | | | | |
| | | | | | | 195 | 200 | | | 205 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Thr | Val | Pro | Ser | Ser | Thr | Trp | Pro | Ser | Glu | Thr | Val | Thr | Cys |
| | | | | | | | | | | | | | | | |
| | | | | | | 210 | 215 | | 220 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Val | Ala | His | Pro | Ala | Ser | Ser | Thr | Lys | Val | Asp | Lys | Lys | Ile | Val |
| | | | | | | | | | | | | | | | |
| | | | | | | 225 | 230 | | 235 | | 240 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Arg | Asp | Cys | Gly | Cys | Lys | Pro | Cys | Ile | Cys | Thr | Val | Pro | Glu | Val |
| | | | | | | | | | | | | | | | |
| | | | | | | 245 | 250 | | 255 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Val | Phe | Ile | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Val | Leu | Thr | Ile |
| | | | | | | | | | | | | | | | |
| | | | | | | 260 | 265 | | 270 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Thr | Pro | Lys | Val | Thr | Cys | Val | Val | Val | Asp | Ile | Ser | Lys | Asp |
| | | | | | | | | | | | | | | | |
| | | | | | | 275 | 280 | | 285 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Pro | Glu | Val | Gln | Phe | Ser | Trp | Phe | Val | Asp | Asp | Val | Glu | Val | His |
| | | | | | | | | | | | | | | | |
| | | | | | | 290 | 295 | | 300 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Gln | Thr | Gln | Pro | Arg | Glu | Glu | Gln | Phe | Asn | Ser | Thr | Phe | Arg |
| | | | | | | | | | | | | | | | |
| | | | | | | 305 | 310 | | 315 | | 320 | | | | |

-continued

Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys
325 330 335

Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu
340 345 350

Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr
355 360 365

Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu
370 375 380

Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp
385 390 395 400

Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile
405 410 415

Met Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln
420 425 430

Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His
435 440 445

Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro
450 455 460

Gly Lys
465

<210> SEQ ID NO 172

<211> LENGTH: 1401

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 172

| | | | | | | |
|-------------|-------------|-------------|------------|------------|-------------|------|
| atgggatgga | gctggacctt | tctttccctc | ctgtcaggaa | ctgcaggtgt | cctctctgag | 60 |
| gtcacaactgc | aacagtctgg | acctgaacta | atgaagcctg | gggcttcagt | gaagatgtcc | 120 |
| tgcaaggcct | ctggatatac | attcaactgac | tacaacatgc | actgggtgaa | gcagaaccaa | 180 |
| ggaaagaccc | tagactggat | aggagaaaatt | aatcctaaca | gtgggtggc | tggctacaac | 240 |
| cagaagttca | agggaaggc | cacattgact | gtagacaagt | cctccaccac | agcctacatg | 300 |
| gagctccgca | gcctgacatc | tgaggactct | gcagtctatt | actgtgcaag | attgggctac | 360 |
| gtatgatatct | acgacgactg | gtacttcgat | gtctggggcg | cagggaccac | ggtacccgtc | 420 |
| tccctagcca | aaacgcacacc | cccatctgtc | tatccactgg | cccctggatc | tgctgccccaa | 480 |
| actaactcca | tggtgaccct | gggatgcctg | gtcaagggct | atttccctga | gccagtgaca | 540 |
| gtgacctgga | actctggatc | cctgtccagc | ggtgtgcaca | cttcccaagc | tgtcctgcag | 600 |
| tctgacctct | acactctgag | cagctcagtg | actgtcccct | ccagcacctg | gcccagcgag | 660 |
| accgtcacct | gcaacgttgc | ccacccggcc | agcagcacca | aggtggacaa | gaaaatttg | 720 |
| cccaggatt | gtgggtgtaa | gccttgcatc | tgtacagtcc | cagaagtatc | atctgtctc | 780 |
| atcttccccc | caaagccaa | ggatgtgtc | accattactc | tgactcttaa | ggtcacgtgt | 840 |
| gttgtgttag | acatcagcaa | ggatgatccc | gaggtccagt | tcagctggtt | tgttagatgt | 900 |
| gtggaggtgc | acacagctca | gacgcaaccc | cgggaggagc | agttcaacag | cactttccgc | 960 |
| tcagtcagtg | aacttcccat | catgcaccag | gactggctca | atggcaagga | gttcaaatgc | 1020 |
| agggtcaaca | gtgcagctt | ccctgcccc | atcgagaaaa | ccatctccaa | aaccaaaggc | 1080 |
| agaccgaagg | ctccacaggt | gtacaccatt | ccacctccca | aggagcagat | ggccaaggat | 1140 |
| aaagtcaagtc | tgacctgcat | gataacagac | ttcttccctg | aagacattac | tgtggagtg | 1200 |
| cagtgaaatg | ggcagccagc | ggagaactac | aagaacactc | agcccatcat | ggacacagat | 1260 |

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```
ggcttact tcatacag caagtcata gtgcagaaga gcaactggga ggcaggaaat    1320
actttacct gctctgtgtt acatgaggcc ctgcacaacc accatactga gaagagcctc    1380
tccccactctc ctggtaaatg a                                         1401
```

<210> SEQ ID NO 173

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 173

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Ile | Thr | Ser | Ser | Leu | Ser | Ala | Ser | Leu | Gly |
| 1 | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Val | Ser | Ile | Ser | Cys | Arg | Ala | Ser | Gln | Asp | Ile | Ser | Asn | Tyr |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | 30 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Trp | Tyr | Gln | Gln | Lys | Pro | Asp | Gly | Thr | Phe | Lys | Leu | Leu | Ile |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | 45 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Tyr | Thr | Ser | Arg | Leu | Phe | Ser | Gly | Val | Pro | Ser | Arg | Phe | Ser | Gly |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | 60 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Gly | Thr | Asp | Tyr | Ser | Leu | Thr | Ile | Tyr | Asn | Leu | Glu | Gln |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | 80 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asp | Phe | Ala | Thr | Tyr | Phe | Cys | Gln | Gln | Gly | Asp | Thr | Leu | Pro | Tyr |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | 95 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Phe | Gly | Gly | Thr | Lys | Val | Glu | Ile | Lys | Arg | Ala | Asp | Ala | Ala | |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | 110 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Thr | Val | Ser | Ile | Phe | Pro | Pro | Ser | Ser | Glu | Gln | Leu | Thr | Ser | Gly |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | 125 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ala | Ser | Val | Val | Cys | Phe | Leu | Asn | Asn | Phe | Tyr | Pro | Lys | Asp | Ile |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | 140 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Val | Lys | Trp | Lys | Ile | Asp | Gly | Ser | Glu | Arg | Gln | Asn | Gly | Val | Leu |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | 160 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Trp | Thr | Asp | Gln | Asp | Ser | Lys | Asp | Ser | Thr | Tyr | Ser | Met | Ser |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | 175 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Leu | Thr | Leu | Thr | Lys | Asp | Glu | Tyr | Glu | Arg | His | Asn | Ser | Tyr |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | 190 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Cys | Glu | Ala | Thr | His | Lys | Thr | Ser | Thr | Ser | Pro | Ile | Val | Lys | Ser |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | 195 | |

| | | | | | |
|-----|-----|-----|-----|-----|-----|
| Phe | Asn | Arg | Asn | Glu | Cys |
| | | | | | |
| | | | | | 210 |

<210> SEQ ID NO 174

<211> LENGTH: 642

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 174

| | | | | | | |
|------------|------------|-------------|------------|-----------|------------|----|
| gatatccaga | tgacacagat | tacatccctcc | ctgtctgcct | ctctggaga | cagggtctcc | 60 |
|------------|------------|-------------|------------|-----------|------------|----|

| | | | | | | |
|------------|------------|-------------|-----------|------------|------------|-----|
| atcagttgca | gggcaagtca | agacatttagc | aattatcaa | atttgtatca | gcagaaacca | 120 |
|------------|------------|-------------|-----------|------------|------------|-----|

| | | | | | | |
|--------------|------------|------------|------------|------------|------------|-----|
| gatggaaacctt | ttaaactcct | tatcttctac | acatcaagat | tattttcagg | agtcccatca | 180 |
|--------------|------------|------------|------------|------------|------------|-----|

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| aggttcagtg | gcagtgggtc | tggAACAGAT | tattctctca | ccatttacaa | cctggagcaa | 240 |
|------------|------------|------------|------------|------------|------------|-----|

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| gaagatTTTG | ccacttactt | ttgccaacag | ggagatacgc | ttccgtacac | tttcggaggg | 300 |
|------------|------------|------------|------------|------------|------------|-----|

| | | | | | | |
|------------|------------|-------------|------------|-------------|------------|-----|
| gggaccaagg | tggAAATAAA | acgggctgtat | gctgcaccaa | ctgttatccat | cttcccacca | 360 |
|------------|------------|-------------|------------|-------------|------------|-----|

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| tccagtgagc | agttaacatc | tggaggtgcc | tcagtcgtgt | gtttcttgaa | caacttctac | 420 |
|------------|------------|------------|------------|------------|------------|-----|

US 9,089,553 B2

191

192

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| | |
|---|-----|
| cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgctctg | 480 |
| aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcact | 540 |
| ttgaccaagg acgagtagtga acgacataac agctataacct gtgaggccac tcacaagaca | 600 |
| tcaacttcac ccattgtcaa gagttcaac aggaatgagt gt | 642 |

<210> SEQ ID NO 175

<211> LENGTH: 234

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 175

| | |
|---|--|
| Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Cys Phe Gln | |
| 1 5 10 15 | |

| | |
|---|--|
| Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ile Thr Ser Ser Leu Ser | |
| 20 25 30 | |

| | |
|---|--|
| Ala Ser Leu Gly Asp Arg Val Ser Ile Ser Cys Arg Ala Ser Gln Asp | |
| 35 40 45 | |

| | |
|---|--|
| Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe | |
| 50 55 60 | |

| | |
|---|--|
| Lys Leu Leu Ile Phe Tyr Thr Ser Arg Leu Phe Ser Gly Val Pro Ser | |
| 65 70 75 80 | |

| | |
|---|--|
| Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Tyr | |
| 85 90 95 | |

| | |
|---|--|
| Asn Leu Glu Gln Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asp | |
| 100 105 110 | |

| | |
|---|--|
| Thr Leu Pro Tyr Thr Phe Gly Gly Thr Lys Val Glu Ile Lys Arg | |
| 115 120 125 | |

| | |
|---|--|
| Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln | |
| 130 135 140 | |

| | |
|---|--|
| Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr | |
| 145 150 155 160 | |

| | |
|---|--|
| Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln | |
| 165 170 175 | |

| | |
|---|--|
| Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr | |
| 180 185 190 | |

| | |
|---|--|
| Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg | |
| 195 200 205 | |

| | |
|---|--|
| His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro | |
| 210 215 220 | |

| | |
|---|--|
| Ile Val Lys Ser Phe Asn Arg Asn Glu Cys | |
| 225 230 | |

<210> SEQ ID NO 176

<211> LENGTH: 702

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 176

| | |
|---|-----|
| atgatgtctt ctgcgtcagtt ccttggcttc ctgttgctct gtttcaagg taccagatgt | 60 |
| gatatccaga tgacacagat tacatccctcc ctgtctgcct ctctggaga cagggtctcc | 120 |
| atcagttgca gggcaagtca agacatttgc aattttttaa attggatcgc gcagaaacca | 180 |
| gatggaaacctt tttaaactcct tatcttctac acatcaagat tattttcagg agtccccatca | 240 |
| aggttcagtg gcagtgggtc tggaacagat tattctctca ccatttacaa cctggagcaa | 300 |

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| | |
|---|-----|
| gaagattttg ccacttactt ttgccaacag ggagatacgc ttccgtacac tttcgaggg | 360 |
| gggaccaagg tggaaataaa acgggctgat gctgcaccaa ctgtatccat cttccacca | 420 |
| tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gttcttgaa caacttctac | 480 |
| cccaaagaca tcaatgtcaa gtgaaagatt gatggcagtg aacgacaaaa tggcgtctg | 540 |
| aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcag | 600 |
| ttgaccaagg acgagttatga acgacataac agctataacct gtgaggccac tcacaagaca | 660 |
| tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gt | 702 |

<210> SEQ ID NO 177

<211> LENGTH: 450

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 177

| | |
|---|--|
| Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly Thr | |
| 1 5 10 15 | |

| | |
|---|--|
| Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr | |
| 20 25 30 | |

| | |
|---|--|
| Asn Met His Trp Val Lys Gln Thr Gln Gly Lys Thr Leu Glu Trp Ile | |
| 35 40 45 | |

| | |
|---|--|
| Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe | |
| 50 55 60 | |

| | |
|---|--|
| Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr | |
| 65 70 75 80 | |

| | |
|---|--|
| Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys | |
| 85 90 95 | |

| | |
|---|--|
| Ala Lys Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val | |
| 100 105 110 | |

| | |
|---|--|
| Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Ala | |
| 115 120 125 | |

| | |
|---|--|
| Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser | |
| 130 135 140 | |

| | |
|---|--|
| Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val | |
| 145 150 155 160 | |

| | |
|---|--|
| Thr Leu Thr Trp Asn Ser Gly Ser Leu Ser Ser Asp Val His Thr Phe | |
| 165 170 175 | |

| | |
|---|--|
| Pro Ala Leu Leu Gln Ser Gly Leu Tyr Thr Leu Ser Ser Ser Val Thr | |
| 180 185 190 | |

| | |
|---|--|
| Val Thr Thr Trp Pro Ser Gln Thr Ile Thr Cys Asn Val Ala His Pro | |
| 195 200 205 | |

| | |
|---|--|
| Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Ser Pro | |
| 210 215 220 | |

| | |
|---|--|
| Thr His Lys Pro Cys Pro Pro Cys Pro Ala Pro Asn Leu Leu Gly Gly | |
| 225 230 235 240 | |

| | |
|---|--|
| Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile | |
| 245 250 255 | |

| | |
|---|--|
| Ser Leu Ser Pro Met Val Thr Cys Val Val Val Asp Val Ser Glu Asp | |
| 260 265 270 | |

| | |
|---|--|
| Asp Pro Asp Val His Val Ser Trp Phe Val Asn Asn Val Glu Val His | |
| 275 280 285 | |

| | |
|---|--|
| Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Ile Arg | |
| 290 295 300 | |

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Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys
305 310 315 320

Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335

Arg Thr Ile Ser Lys Pro Lys Gly Pro Val Arg Ala Pro Gln Val Tyr
340 345 350

Val Leu Pro Pro Pro Glu Glu Met Thr Lys Lys Gln Val Thr Leu
355 360 365

Thr Cys Met Ile Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp
370 375 380

Thr Asn Asn Gly Gln Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu
405 410 415

Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His
420 425 430

Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro
435 440 445

Gly Lys
450

<210> SEQ ID NO 178

<211> LENGTH: 1350

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 178

| | | | | | | |
|-------------|---------------|------------|-------------|-------------|------------|------|
| gagggtccaa | tgcaacagtc | tggacctgaa | ctaatgaagc | ctgggacttc | agtgaagatg | 60 |
| tccctgcagg | tttctggata | tacattca | ctactacaaca | tgcactgggt | gaagcagacc | 120 |
| caaggaaaga | cccttagatg | gataggagaa | attaatccta | acagtgggtt | tgctggctac | 180 |
| aaccagaagt | tcaaggggcaa | ggccacattt | actgttagaca | agtccctcac | cacagcctac | 240 |
| atggagctcc | gcagectgac | atctgaggac | tctgcagtct | attactgtgc | aaaattgggc | 300 |
| tacgatgata | tctacgacga | ctggattttc | gatgtctggg | gcccaggac | cacggtcacc | 360 |
| gtctcctcag | ccaaaacaac | agccccatcg | gtctatccac | tggccctgt | gtgtggagat | 420 |
| acaactggct | cctcggtgac | tctaggatgc | ctggtaagg | gttattccc | tgagccagt | 480 |
| accttgacct | ggaactctgg | atccctgtcc | agtgtatgtc | acaccttccc | agctctcctg | 540 |
| cagtctggcc | tctacaccct | cagcagctca | gtgactgtaa | ccacctggcc | cagccagacc | 600 |
| atcacctgca | atgtggccca | cccgccaagc | agcaccaaag | tggacaagaa | aattgagccc | 660 |
| agagggtccc | caacacataa | accctgtct | ccatgccag | ctccctaacct | cttgggttga | 720 |
| ccatccgtct | tcatcttccc | tccaaagatc | aaggatgtac | tcatgtatctc | cctgagcccc | 780 |
| atgggtcacgt | gtgtgggtgt | ggatgtgac | gaggatgacc | catatgtcca | tgtcagctgg | 840 |
| ttcgtgaaca | acgtgaaagt | acacacagct | cagacacaaa | cccatagaga | ggattacaac | 900 |
| agtactatcc | gggtggtcag | tgcctccccc | atccagcacc | aggactggat | gagtgccaa | 960 |
| gagttcaa | at gcaaggtaaa | caacaaagcc | ctcccagcgc | ccatcgagag | aaccatctca | 1020 |
| aaacccaaag | ggccagtaag | agctccacag | gtatatgtct | tgcctccacc | agaagaagag | 1080 |
| atgactaaga | aacaggtaac | tctgacctgc | atgatcacag | acttcatgcc | tgaagacatt | 1140 |
| tacgtggagt | ggaccaacaa | cggccaaaca | gagctaaact | acaagaacac | tgaaccagt | 1200 |
| ctggactctg | atggttctta | cttcatgtac | agcaagctga | gagtgaaaa | gaagaactgg | 1260 |

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gtggaaagaa atagctactc ctgttcagtg gtccacgagg gtctgcacaa tcaccacacg 1320
 actaagagct tctccggac tccgggtaaa 1350

<210> SEQ ID NO 179
 <211> LENGTH: 469
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 179

Met Gly Trp Ser Trp Thr Phe Leu Leu Ser Gly Thr Ala Gly
 1 5 10 15

Val Leu Ser Glu Val Gln Leu Gln Ser Gly Pro Glu Leu Met Lys
 20 25 30

Pro Gly Thr Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Asp Tyr Asn Met His Trp Val Lys Gln Thr Gln Gly Lys Thr Leu
 50 55 60

Glu Trp Ile Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn
 65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr
 85 90 95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Tyr Cys Ala Lys Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr
 115 120 125

Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Ser Ser Ala Lys
 130 135 140

Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr
 145 150 155 160

Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro
 165 170 175

Glu Pro Val Thr Leu Thr Trp Asn Ser Gly Ser Leu Ser Ser Asp Val
 180 185 190

His Thr Phe Pro Ala Leu Leu Gln Ser Gly Leu Tyr Thr Leu Ser Ser
 195 200 205

Ser Val Thr Val Thr Trp Pro Ser Gln Thr Ile Thr Cys Asn Val
 210 215 220

Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg
 225 230 235 240

Gly Ser Pro Thr His Lys Pro Cys Pro Pro Cys Pro Ala Pro Asn Leu
 245 250 255

Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val
 260 265 270

Leu Met Ile Ser Leu Ser Pro Met Val Thr Cys Val Val Val Asp Val
 275 280 285

Ser Glu Asp Asp Pro Asp Val His Val Ser Trp Phe Val Asn Asn Val
 290 295 300

Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser
 305 310 315 320

Thr Ile Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met
 325 330 335

Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala
 340 345 350

US 9,089,553 B2

199

200

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ile | Glu | Arg | Thr | Ile | Ser | Lys | Pro | Lys | Gly | Pro | Val | Arg | Ala | Pro |
| 355 | | | | | | | | | | | | | | | 365 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Tyr | Val | Leu | Pro | Pro | Pro | Glu | Glu | Glu | Met | Thr | Lys | Lys | Gln |
| 370 | | | | | | | | | | | | | | | 380 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Leu | Thr | Cys | Met | Ile | Thr | Asp | Phe | Met | Pro | Glu | Asp | Ile | Tyr |
| 385 | | | | | | | | | | | | | | | 400 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Trp | Thr | Asn | Asn | Gly | Gln | Thr | Glu | Leu | Asn | Tyr | Lys | Asn | Thr |
| 405 | | | | | | | | | | | | | | | 415 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Pro | Val | Leu | Asp | Ser | Asp | Gly | Ser | Tyr | Phe | Met | Tyr | Ser | Lys | Leu |
| 420 | | | | | | | | | | | | | | | 430 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Val | Glu | Lys | Lys | Asn | Trp | Val | Glu | Arg | Asn | Ser | Tyr | Ser | Cys | Ser |
| 435 | | | | | | | | | | | | | | | 445 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | His | Glu | Gly | Leu | His | Asn | His | His | Thr | Thr | Lys | Ser | Phe | Ser |
| 450 | | | | | | | | | | | | | | | 460 |

| | | | | |
|-----|-----|-----|-----|-----|
| Arg | Thr | Pro | Gly | Lys |
| 465 | | | | |

<210> SEQ_ID NO 180

<211> LENGTH: 1407

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 180

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| atgggatgga | gctggacctt | tctttcctc | ctgtcaggaa | ctgcaggtgt | cctctctgag | 60 |
| gtccaaactgc | aacagtctgg | acctgaacta | atgaagcctg | ggacttcagt | gaagatgtcc | 120 |
| tgcaaggctt | ctggatatac | attcaactgac | tacaacatgc | actgggtgaa | gcagacccaa | 180 |
| ggaaagaccc | tagagtggat | aggagaaatt | aatcctaaca | gtgggtggtc | tggctacaac | 240 |
| cagaagtta | agggcaaggc | cacattgact | gtagacaagt | cctccaccac | agcctacatg | 300 |
| gagctccgca | gcctgacatc | tgaggactct | gcagtctatt | actgtgcaaa | attggctac | 360 |
| gatgatatact | acgacgactg | gtatbtcgt | gtctggggcg | cagggaccac | ggtcacccgtc | 420 |
| tcctcagcca | aaacaacagc | cccatcggtc | tatccactgg | cccctgtgtg | tggagataca | 480 |
| actggctct | cggtgactct | aggatgcctg | gtcaagggtt | atttccctga | gccagtgacc | 540 |
| ttgacctgga | actctggatc | cctgtccagt | gatgtgcaca | cttcccaagc | tctctgcag | 600 |
| tctggctct | acaccctcag | cagctcagtg | actgttaacc | cctggcccaag | ccagaccatc | 660 |
| acctgcaatg | tggcccaccc | ggcaagcagc | accaaagtgg | acaagaaaat | tgagcccaga | 720 |
| gggtccccaa | cacataaacc | ctgtcctcca | tgcccgatctc | ctaacccttt | gggtggacca | 780 |
| tccgttca | tctccctcc | aaagatcaag | gatgtactca | tgatctccct | gagccccatg | 840 |
| gtcacgttg | tggtggtgga | tgtgagcag | gatgaccctg | atgtccatgt | cagctggttc | 900 |
| gtgaacaacg | tggaagtaca | cacagctcg | acacaaaccc | atagagagga | ttacaacagt | 960 |
| actatccggg | tggtcagtgc | cctcccccato | cagcaccagg | actggatgag | tggcaaggag | 1020 |
| ttcaaatgca | aggtcaacaa | caaagccctc | ccagcgccca | tcgagagaac | catctcaaaa | 1080 |
| ccaaaggcc | cagtaagagc | tccacaggt | tatgtcttc | ctccaccaga | agaagagatg | 1140 |
| actaagaaac | aggtcaactct | gacctgcatg | atcacagact | tcatgcctga | agacatttac | 1200 |
| gtggagtgga | ccaacaacgg | gcaaacagag | ctaaactaca | agaacactga | accagtctg | 1260 |
| gactctgtat | gttcttactt | catgtacagc | aagctgagag | tggaaaagaa | gaactgggtg | 1320 |
| gaaagaata | gctactcctg | ttcagtggtc | cacgagggtc | tgcacaatca | ccacacgact | 1380 |
| aagagcttct | cccgactcc | gggtaaaa | | | | 1407 |

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<210> SEQ_ID NO 181
<211> LENGTH: 214
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 181

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Thr | Thr | Ser | Ser | Leu | Ser | Ala | Ser | Leu | Gly |
| 1 | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Val | Ser | Ile | Ser | Cys | Arg | Ala | Ser | Gln | Asp | Ile | Ser | Asn | Tyr |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | 30 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Trp | Tyr | Gln | Gln | Lys | Pro | Asp | Gly | Thr | Phe | Lys | Leu | Leu | Ile |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | 45 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Tyr | Thr | Ser | Arg | Leu | Leu | Ser | Gly | Val | Pro | Ser | Arg | Phe | Ser | Gly |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | 50 | 60 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Gly | Thr | Asp | Tyr | Ser | Leu | Thr | Ile | Tyr | Asn | Leu | Glu | Gln |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | 65 | 80 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asp | Phe | Ala | Thr | Tyr | Phe | Cys | Gln | Gln | Gly | Asp | Thr | Leu | Pro | Tyr |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | 85 | 95 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Phe | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg | Ala | Asp | Ala | Ala | |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | 100 | 110 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Thr | Val | Ser | Ile | Phe | Pro | Leu | Ser | Ser | Glu | Gln | Leu | Thr | Ser | Gly |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | 115 | 125 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ala | Ser | Val | Val | Cys | Phe | Leu | Asn | Asn | Phe | Tyr | Pro | Lys | Asp | Ile |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | 130 | 140 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Val | Lys | Trp | Lys | Ile | Asp | Gly | Ser | Glu | Arg | Gln | Asn | Gly | Val | Leu |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | 145 | 160 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Trp | Thr | Asp | Gln | Asp | Ser | Lys | Asp | Ser | Thr | Tyr | Ser | Met | Ser |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | 165 | 175 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Leu | Thr | Leu | Thr | Lys | Asp | Glu | Tyr | Glu | Arg | His | Asn | Ser | Tyr |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | 180 | 190 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Cys | Glu | Ala | Thr | His | Lys | Thr | Ser | Thr | Ser | Pro | Ile | Val | Lys | Ser |
| | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | 195 | 205 | |

Phe Asn Arg Asn Glu Cys
210

<210> SEQ_ID NO 182
<211> LENGTH: 645
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 182

| | | | | | | |
|------------|------------|------------|------------|-----------|------------|----|
| gatatccaga | tgacacagac | tacatcctcc | ctgtctgcct | ctctggaga | cagggtctcc | 60 |
|------------|------------|------------|------------|-----------|------------|----|

| | | | | | | |
|------------|-------------|------------|-----------|--------------|------------|-----|
| atcagtgtca | gggcagaatgc | agacatttgc | aatttttaa | actggatataca | gcagaaacca | 120 |
|------------|-------------|------------|-----------|--------------|------------|-----|

| | | | | | | |
|--------------|-------------|------------|------------|------------|-------------|-----|
| gatggaaacctt | ttaaacttcct | tatcttctac | acatcaagat | tactctcagg | agtccccatca | 180 |
|--------------|-------------|------------|------------|------------|-------------|-----|

| | | | | | | |
|------------|------------|-----------|-----------|----------|------------|-----|
| aggtttcagg | gcagtggttc | tggaaacat | tttgcacat | ccatccat | cctggagcaa | 240 |
|------------|------------|-----------|-----------|----------|------------|-----|

| | | | | | | |
|------------|------------|------------|------------|------------|-----------|-----|
| gaagattttg | ccacttactt | ttgccaacat | ggagatacgc | ttccgtacac | tttcggagg | 300 |
|------------|------------|------------|------------|------------|-----------|-----|

| | | | | | | |
|------------|-------------|------------|------------|-------------|------------|-----|
| gggaccaaac | tggaaaataaa | acggggctgt | gctgcaccaa | ctgttatccat | cttcccacta | 360 |
|------------|-------------|------------|------------|-------------|------------|-----|

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| tccagtgagc | agttAACATC | tggaggtgtc | tcagtcgtgt | gtttcttgaa | caacttctac | 420 |
|------------|------------|------------|------------|------------|------------|-----|

| | | | | | | |
|-------------|------------|-------------|------------|------------|-----------|-----|
| cccaaaggaca | tcaatgtcaa | gtggaaagatt | gatggcagtg | aacgacaaaa | tggcgtctg | 480 |
|-------------|------------|-------------|------------|------------|-----------|-----|

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| aacagttgga | ctgatcagga | cagcaaaagac | agcacctaca | gcatgagcag | caccctcact | 540 |
|------------|------------|-------------|------------|------------|------------|-----|

| | | | | | | |
|------------|-------------|------------|-------------|------------|------------|-----|
| ttgaccaagg | acgagttatga | acgacataac | agctataacct | gtgaggccac | tcacaagaca | 600 |
|------------|-------------|------------|-------------|------------|------------|-----|

US 9,089,553 B2

203

204

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| | |
|--|-----|
| tcaacttcac ccattgtcaa gagttcaac aggaatgagt gttag | 645 |
|--|-----|

<210> SEQ ID NO 183
<211> LENGTH: 234
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 183

| | |
|---|--|
| Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Cys Phe Gln | |
| 1 5 10 15 | |
| Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser | |
| 20 25 30 | |
| Ala Ser Leu Gly Asp Arg Val Ser Ile Ser Cys Arg Ala Ser Gln Asp | |
| 35 40 45 | |
| Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe | |
| 50 55 60 | |
| Lys Leu Leu Ile Phe Tyr Thr Ser Arg Leu Leu Ser Gly Val Pro Ser | |
| 65 70 75 80 | |
| Arg Phe Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Tyr | |
| 85 90 95 | |
| Asn Leu Glu Gln Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asp | |
| 100 105 110 | |
| Thr Leu Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg | |
| 115 120 125 | |
| Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Leu Ser Ser Glu Gln | |
| 130 135 140 | |
| Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr | |
| 145 150 155 160 | |
| Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln | |
| 165 170 175 | |
| Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr | |
| 180 185 190 | |
| Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg | |
| 195 200 205 | |
| His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro | |
| 210 215 220 | |
| Ile Val Lys Ser Phe Asn Arg Asn Glu Cys | |
| 225 230 | |

<210> SEQ ID NO 184
<211> LENGTH: 705
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 184

| | |
|--|-----|
| atgatgtcct ctgctcagg ttctgggtcc ctgttgctct gttttcaagg taccagatgt | 60 |
| gatatatccaga tgacacagac tacatcctcc ctgtctgcct ctctgggaga cagggtctcc | 120 |
| atcagttgca gggcaagtca agacatttgc aattatattaa actggatata gcagaaaccca | 180 |
| gatggaaacctt ttaaactcct tatcttctac acatcaagat tactctcagg agtccccatca | 240 |
| aggttcaggc gcagtggttc tggAACAGAT tattctctca ccatttacaa cctggagcaa | 300 |
| gaagatTTG ccacttactt ttgccaacag ggagatacgc ttccgtacac tttcggaggg | 360 |
| gggaccaaac tggAAATAAA acgggctgtat gctgcaccaa ctgttatccat cttcccacta | 420 |
| tccaggtagc agttaacatc tggagggtgcc tcagtcgtgt gtttttgaa caacttctac | 480 |

US 9,089,553 B2

205**206**

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| | |
|---|-----|
| cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa tggcgctctg | 540 |
| aacagttgga ctgatcgaga cagcaaagac agcacctaca gcatgagcag caccctcact | 600 |
| ttgaccaagg acgagtagtga acgacataac agctataacct gtgaggccac tcacaagaca | 660 |
| tcaacttcac ccattgtcaa gagttcaac aggaatgagt gtttg | 705 |

<210> SEQ ID NO 185

<211> LENGTH: 447

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 185

| | | | |
|---|---|----|----|
| Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly Ala | | | |
| 1 | 5 | 10 | 15 |

| | | | |
|---|----|----|--|
| Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr | | | |
| 20 | 25 | 30 | |

| | | | |
|---|----|----|--|
| Asn Met His Trp Val Lys Gln Asn Gln Gly Lys Thr Leu Glu Trp Ile | | | |
| 35 | 40 | 45 | |

| | | | |
|---|----|----|--|
| Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe | | | |
| 50 | 55 | 60 | |

| | | | |
|---|----|----|----|
| Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr | | | |
| 65 | 70 | 75 | 80 |

| | | | |
|---|----|----|--|
| Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys | | | |
| 85 | 90 | 95 | |

| | | | |
|---|-----|-----|--|
| Ala Arg Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val | | | |
| 100 | 105 | 110 | |

| | | | |
|---|-----|-----|--|
| Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Pro | | | |
| 115 | 120 | 125 | |

| | | | |
|---|-----|-----|--|
| Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser | | | |
| 130 | 135 | 140 | |

| | | | |
|---|-----|-----|-----|
| Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val | | | |
| 145 | 150 | 155 | 160 |

| | | | |
|---|-----|-----|--|
| Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe | | | |
| 165 | 170 | 175 | |

| | | | |
|---|-----|-----|--|
| Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Val Thr | | | |
| 180 | 185 | 190 | |

| | | | |
|---|-----|-----|--|
| Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala | | | |
| 195 | 200 | 205 | |

| | | | |
|---|-----|-----|--|
| His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp | | | |
| 210 | 215 | 220 | |

| | | | |
|---|-----|-----|-----|
| Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val | | | |
| 225 | 230 | 235 | 240 |

| | | | |
|---|-----|-----|--|
| Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr | | | |
| 245 | 250 | 255 | |

| | | | |
|---|-----|-----|--|
| Pro Lys Val Thr Cys Val Val Asp Ile Ser Lys Asp Asp Pro Glu | | | |
| 260 | 265 | 270 | |

| | | | |
|---|-----|-----|--|
| Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln | | | |
| 275 | 280 | 285 | |

| | | | |
|---|-----|-----|--|
| Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser | | | |
| 290 | 295 | 300 | |

| | | | |
|---|-----|-----|-----|
| Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys | | | |
| 305 | 310 | 315 | 320 |

| | | | |
|---|-----|-----|--|
| Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile | | | |
| 325 | 330 | 335 | |

-continued

Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro
340 345 350

Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met
355 360 365

Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn
370 375 380

Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr
385 390 395 400

Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn
405 410 415

Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu
420 425 430

His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
435 440 445

<210> SEQ ID NO 186

<211> LENGTH: 1344

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 186

gaggtccaaac tgcaaacagtc tggacctgaa ctaatgaagg ctgggggttc agtgaagatg 60
 tcctgcaagg cttctggata tacattcact gactacaaca tgcactgggt gaagcagaac 120
 caaggaaaaga ccctagaatg gataggagaa attaatccta acagtgggtgg tgctggctac 180
 aaccagaagt tcaaggccaa ggccacattt actgttagaca agtcctccac cacagcctac 240
 atggagctcc gcagectgac atctgaggac tctgcagtct attactgtgc aagattggc 300
 tacgatgata tctacgacga ctggacttc gatgtctggg ggcgcaggagcac cacggtcacc 360
 gtctccctcg ccaaaacgac acccccattt gtctatccac tggcccttgg atctgctgcc 420
 caaaactaact ccatggtgac cctgggatgc ctggtaagg gctatttccc tgagccatgt 480
 acagtgacct ggaactctgg atccctgtcc agccgtgtgc acacccccc agctgtctg 540
 cagtcgtacc tctacactct gaggcgtca gtgactgtcc cttccagcac ctggcccgac 600
 gagacccgtca cctgcaacgt tgcccacccg gccagcagca ccaagggtgga caagaaaatt 660
 gtgcccaggg atttgtgggg taaggcatttc atatgtacag tccccaaatgt atcatctgtc 720
 ttcatcttcc ccccaaagcc caaggatgtg ctcaccatta ctctgactcc taaggtcacg 780
 tgtgttgtgg tagacatcg caaggatgtt cccgagggtcc agttcagctg gtttttagat 840
 gatgtggagg tgcacacagc tcagacgcaa ccccgaggagg agcagttcaa cagcacttcc 900
 cgctcagtca gtgaacttcc catcatgcac caggactggc tcaatggcaa ggagttcaaa 960
 tgcagggtca acagtgcagc tttccctgccc cccatcgaga aaaccatctc caaaaccaaa 1020
 ggcagacccga aggctccaca ggtgtacacc attccacccctt ccaaggagca gatggccaag 1080
 gataaaagtca gtctgacctg catgataaca gacttcttcc ctgaagacat tactgtggag 1140
 tggcagtgga atgggcagcc agcggagaac tacaagaaca ctcagcccat catggacaca 1200
 gatggcttctt acttcatctta cagcaagctc aatgtgcaga agagcaactg ggaggcagga 1260
 aataactttca cctgctctgt gttacatgag ggcctgcaca accaccatac tgagaagagc 1320
 ctctcccaact ctcctggtaa atga 1344

<210> SEQ ID NO 187

<211> LENGTH: 466

<212> TYPE: PRT

-continued

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 187

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Trp | Ser | Trp | Thr | Phe | Leu | Phe | Leu | Leu | Ser | Gly | Thr | Ala | Gly |
| 1 | | | | | | | | | | | | | | | |
| | | | | | | | 5 | | 10 | | | | 15 | | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ser | Glu | Val | Gln | Leu | Gln | Ser | Gly | Pro | Glu | Leu | Met | Lys |
| | | | | | | | | | | | | | | |
| | | | | | | | 20 | | 25 | | | | 30 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Ala | Ser | Val | Lys | Met | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe |
| | | | | | | | | | | | | | | | |
| | | | | | | | 35 | | 40 | | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asp | Tyr | Asn | Met | His | Trp | Val | Lys | Gln | Asn | Gln | Gly | Lys | Thr | Leu |
| | | | | | | | | | | | | | | | |
| | | | | | | | 50 | | 55 | | | 60 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Trp | Ile | Gly | Glu | Ile | Asn | Pro | Asn | Ser | Gly | Gly | Ala | Gly | Tyr | Asn |
| | | | | | | | | | | | | | | | |
| | | | | | | | 65 | | 70 | | 75 | | 80 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Lys | Phe | Lys | Gly | Lys | Ala | Thr | Leu | Thr | Val | Asp | Lys | Ser | Ser | Thr |
| | | | | | | | | | | | | | | | |
| | | | | | | | 85 | | 90 | | | 95 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Tyr | Met | Glu | Leu | Arg | Ser | Leu | Thr | Ser | Glu | Asp | Ser | Ala | Val |
| | | | | | | | | | | | | | | | |
| | | | | | | | 100 | | 105 | | | 110 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Cys | Ala | Arg | Leu | Gly | Tyr | Asp | Asp | Ile | Tyr | Asp | Asp | Trp | Tyr |
| | | | | | | | | | | | | | | | |
| | | | | | | | 115 | | 120 | | | 125 | | | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Asp | Val | Trp | Gly | Ala | Gly | Thr | Val | Thr | Val | Ser | Ser | Ala | Lys |
| | | | | | | | | | | | | | | |
| | | | | | | | 130 | | 135 | | | 140 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Thr | Pro | Pro | Ser | Val | Tyr | Pro | Leu | Ala | Pro | Gly | Ser | Ala | Ala | Gln |
| | | | | | | | | | | | | | | | |
| | | | | | | | 145 | | 150 | | 155 | | 160 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asn | Ser | Met | Val | Thr | Leu | Gly | Cys | Leu | Val | Lys | Gly | Tyr | Phe | Pro |
| | | | | | | | | | | | | | | | |
| | | | | | | | 165 | | 170 | | | 175 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Pro | Val | Thr | Val | Thr | Trp | Asn | Ser | Gly | Ser | Leu | Ser | Ser | Gly | Val |
| | | | | | | | | | | | | | | | |
| | | | | | | | 180 | | 185 | | | 190 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser | Asp | Leu | Tyr | Thr | Leu | Ser | Ser |
| | | | | | | | | | | | | | | | |
| | | | | | | | 195 | | 200 | | | 205 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Thr | Val | Pro | Ser | Ser | Thr | Trp | Pro | Ser | Glu | Thr | Val | Thr | Cys |
| | | | | | | | | | | | | | | | |
| | | | | | | | 210 | | 215 | | | 220 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Val | Ala | His | Pro | Ala | Ser | Ser | Thr | Lys | Val | Asp | Lys | Lys | Ile | Val |
| | | | | | | | | | | | | | | | |
| | | | | | | | 225 | | 230 | | | 235 | | 240 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Arg | Asp | Cys | Gly | Cys | Lys | Pro | Cys | Ile | Cys | Thr | Val | Pro | Glu | Val |
| | | | | | | | | | | | | | | | |
| | | | | | | | 245 | | 250 | | | 255 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Val | Phe | Ile | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Val | Leu | Thr | Ile |
| | | | | | | | | | | | | | | | |
| | | | | | | | 260 | | 265 | | | 270 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Thr | Pro | Lys | Val | Thr | Cys | Val | Val | Val | Asp | Ile | Ser | Lys | Asp |
| | | | | | | | | | | | | | | | |
| | | | | | | | 275 | | 280 | | | 285 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asp | Pro | Glu | Val | Gln | Phe | Ser | Trp | Phe | Asp | Asp | Val | Glu | Val | His | |
| | | | | | | | | | | | | | | | |
| | | | | | | | 290 | | 295 | | | 300 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Gln | Thr | Gln | Pro | Arg | Glu | Glu | Gln | Phe | Asn | Ser | Thr | Phe | Arg |
| | | | | | | | | | | | | | | | |
| | | | | | | | 305 | | 310 | | | 315 | | 320 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Ser | Glu | Leu | Pro | Ile | Met | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys |
| | | | | | | | | | | | | | | | |
| | | | | | | | 325 | | 330 | | | 335 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Phe | Lys | Cys | Arg | Val | Asn | Ser | Ala | Ala | Phe | Pro | Ala | Pro | Ile | Glu |
| | | | | | | | | | | | | | | | |
| | | | | | | | 340 | | 345 | | | 350 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Thr | Ile | Ser | Lys | Thr | Lys | Gly | Arg | Pro | Lys | Ala | Pro | Gln | Val | Tyr |
| | | | | | | | | | | | | | | | |
| | | | | | | | 355 | | 360 | | | 365 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Ile | Pro | Pro | Lys | Glu | Gln | Met | Ala | Lys | Asp | Lys | Val | Ser | Leu | |
| | | | | | | | | | | | | | | | |
| | | | | | | | 370 | | 375 | | | 380 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Cys | Met | Ile | Thr | Asp | Phe | Phe | Pro | Glu | Asp | Ile | Thr | Val | Glu | Trp |
| | | | | | | | | | | | | | | | |
| | | | | | | | 385 | | 390 | | | 395 | | 400 | |

-continued

Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile
405 410 415

Met Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln
420 425 430

Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His
435 440 445

Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro
450 455 460

Gly Lys
465

<210> SEQ ID NO 188

<211> LENGTH: 1401

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 188

| | | | | | | |
|-------------|--------------|-------------|-------------|-------------|------------|------|
| atgggatgga | gtctggacattt | tcttttcttc | ctgtcaggaa | ctgcaggtgt | cctctctgag | 60 |
| gtcccaactgc | aacagtctgg | acctgaacta | atgaagcctg | gggcttcagt | gaagatgtcc | 120 |
| tgcaaggctt | ctggatatac | attcaactgac | tacaacatgc | actgggtgaa | gcagaaccaa | 180 |
| ggaaagaccc | tagaatggat | aggagaaaatt | aatcctaaca | gtgggttgtc | tggctacaac | 240 |
| cagaagtca | agggcaaggc | cacattgact | gtagacaagt | cctccaccac | agcctacatg | 300 |
| gagctccgca | gcctgacate | tgaggactct | gcagtctatt | actgtgcaag | attgggctac | 360 |
| gtatgatatct | acgacgactg | gtacttcgtat | gtctggggcg | cagggaccac | ggtcaccgtc | 420 |
| tcctcagcca | aaacgacacc | cccatctgtc | tatccactgg | cccctggatc | tgctgccaa | 480 |
| actaactcca | ttgtgacccct | gggatgcctg | gtcaagggtc | atttccctga | gccagtgaca | 540 |
| gtgacctgga | actctggatc | cctgtccagc | ggtgtgcaca | cttcccagc | tgtctgcag | 600 |
| tctgacactct | acactctgag | cagtcagtg | actgtccccct | ccagcacctg | gcccagcgcg | 660 |
| accgtcacct | gcaacgttgc | ccacccggcc | agcagcacca | aggtggacaa | gaaaatttgt | 720 |
| cccgaggatt | gtgggtgtaa | gccttgcata | tgtacagtcc | cagaagtatc | atctgtcttc | 780 |
| atcttcccc | caaagccaa | ggatgtgtc | accattactc | tgactctaa | ggtcacgtgt | 840 |
| gttgggttag | acatcagcaa | ggatgtatccc | gaggtccagt | tcaagctggtt | tgttagatgt | 900 |
| gtggaggtgc | acacagctca | gacgcaaccc | cgggaggagc | agttcaacag | cactttccgc | 960 |
| tcagtcagtg | aacttccat | catgcaccag | gactggctca | atggcaagga | gttcaaatgc | 1020 |
| agggtcaaca | gtgcagcttt | ccctgcccc | atcgagaaaa | ccatctccaa | aaccaaaggc | 1080 |
| agaccgaagg | ctccacaggt | gtacaccatt | ccacccccc | aggagcagat | ggccaaggat | 1140 |
| aaagtcaatc | tgacctgtcat | gataacagac | ttttccctg | aagacattac | tgtggagtg | 1200 |
| cagttggaaat | ggcagccagc | ggagaactac | aagaacactc | agcccatcat | ggacacagat | 1260 |
| ggctcttaatc | tcatctacag | caagctcaat | gtgcagaaga | gcaactggga | ggcaggaaat | 1320 |
| actttcacct | gtctgtgtt | acatgagggc | ctgcacaacc | accataactga | gaagagcctc | 1380 |
| tccactctc | ctggtaatg | a | | | | 1401 |

<210> SEQ ID NO 189

<211> LENGTH: 213

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 189

-continued

Gln Ile Val Leu Ser Gln Ser Pro Ala Phe Leu Ser Val Ser Pro Gly
1 5 10 15

Asp Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Ile Ser Tyr Ile
20 25 30

His Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Arg Ser Trp Ile Tyr
35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Gly Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asp Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala Pro
100 105 110

Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly
115 120 125

Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn
130 135 140

Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn
145 150 155 160

Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
165 170 175

Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr
180 185 190

Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe
195 200 205

Asn Arg Asn Glu Cys
210

<210> SEQ ID NO 190
<211> LENGTH: 642
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 190

```
caaattgttc tctcccaagtc tccagcattc ctgtctgtat ctccaggggtaaagggtcaca 60
atgacttgca gggccagctc aagtataagt tacatacact ggtttcagca gaagccagga 120
tccctccccca gatcctggat ttatgccaca tccaacctgg cttctggagt ccctggtcgc 180
ttcagtgccca gtgggtctgg gacctttac tctctcacaa tcagcagagt ggaggctgag 240
gatgctgcca cttattactg ccagcagtgg agtagtgacc cactcacgtt cggtgctgg 300
accaagctgg agctgaaacg ggctgatgtc gcaccaactg tatccatctt cccaccatcc 360
agtgagcagt taacatctgg aggtgcctca gtcgtgtgct tcttgaacaa cttctacccc 420
aaagacatca atgtcaagtg gaagattgtat ggcagtgtaaac gacaaaatgg cgtcctgtaa 480
agttggactg atcaggacag caaagacacg acctacagca tgagcagcac cctcacgtt 540
accaaggacg agtatgaacg acataacacg tatacctgtg aggccactca caagacatca 600
acttcaccca ttgtcaagag cttcaacagg aatgagttt ag 642
```

<210> SEQ ID NO 191
<211> LENGTH: 235
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 191

-continued

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Phe
 20 25 30
 Leu Ser Val Ser Pro Gly Asp Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Ile Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Arg Ser Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Gly Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Ser Asp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
 130 135 140
 Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
 145 150 155 160
 Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
 165 170 175
 Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
 180 185 190
 Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
 195 200 205
 Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
 210 215 220
 Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 225 230 235

<210> SEQ_ID NO 192
 <211> LENGTH: 708
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <400> SEQUENCE: 192

```

atggattttc aagtgcagat tttcagcttc ctgctaataca gtgtttcagg cataatgtcc 60
agaggacaaa ttgttctctc ccagtctcca gcattccgt ctgttatctcc aggggataag 120
gtcacaatga cttgcagggc cagctcaagt ataagttaca tacactgggt tcagcagaag 180
ccaggatcct cccccagatc ctggatttat gccacatcca acctggcttc tggagtccct 240
ggtcgcttca gtggcagtgg gtctgggacc tcttactctc tcacaatcag cagagtggag 300
gtcgaggatc ctgccactta ttactgccag cagtgaggta gtgaccact cacgttcgg 360
gttgggacca agctggagct gaaacgggct gatgctgcac caactgtatc catctccca 420
ccatccagtgc acgatgttaac atctggaggt gcctcagtgc tggcttctt gaacaacttc 480
taccccaaag acatcaatgt caagtggaaat ttgtatggca gtgaacgaca aaatggcg 540
ctgaacagtt ggactgatca ggacagcaaa gacagcacct acagcatgag cagcaccctc 600
acgttgcacca aggacgagta tgaacgcacat aacagctata cctgtgaggc cactcacaag 660
acatcaactt cacccattgt caagagcttc aacaggaatg agtgttag 708
  
```

-continued

<210> SEQ ID NO 193
 <211> LENGTH: 445
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 193

```

Glu Val Gln Leu Gln Gln Ser Gly Ala Asp Leu Val Gln Pro Gly Ala
1           5           10          15

Ser Val Lys Val Ser Cys Thr Ala Ser Gly Phe Asp Ile Lys Asp Tyr
20          25          30

Tyr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Glu Trp Ile
35          40          45

Gly Arg Val Asp Pro Asp Asn Gly Glu Thr Glu Phe Ala Pro Lys Phe
50          55          60

Pro Gly Lys Ala Thr Phe Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65          70          75          80

Leu Gln Leu Arg Gly Leu Thr Ser Glu Asp Thr Ala Ile Tyr Tyr Cys
85          90          95

Gly Arg Glu Asp Tyr Asp Gly Thr Tyr Thr Trp Phe Pro Tyr Trp Gly
100         105         110

Gln Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser
115         120         125

Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val
130         135         140

Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val
145         150         155         160

Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala
165         170         175

Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro
180         185         190

Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro
195         200         205

Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
210         215         220

Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile
225         230         235         240

Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys
245         250         255

Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln
260         265         270

Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln
275         280         285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu
290         295         300

Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg
305         310         315         320

Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
325         330         335

Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro
340         345         350

Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr
355         360         365

Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
370         375         380

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US 9,089,553 B2

219**220**

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | Glu | Asn | Tyr | Lys | Asn | Thr | Gln | Pro | Ile | Met | Asp | Thr | Asp | Gly |
| 385 | | | | | 390 | | | | 395 | | | | | | 400 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Tyr | Phe | Ile | Tyr | Ser | Lys | Leu | Asn | Val | Gln | Lys | Ser | Asn | Trp | Glu |
| | | | | | 405 | | | 410 | | | | | | | 415 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gly | Asn | Thr | Phe | Thr | Cys | Ser | Val | Leu | His | Glu | Gly | Leu | His | Asn |
| | | | | | | 420 | | 425 | | | | | | | 430 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| His | His | Thr | Glu | Lys | Ser | Leu | Ser | His | Ser | Pro | Gly | Lys | | |
| | | | | | 435 | | 440 | | | | | | | 445 |

<210> SEQ ID NO 194

<211> LENGTH: 1338

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 194

| | | | | | | |
|--------------|-------------|--------------|--------------|------------|-------------|------|
| gaagttcagc | tgcaacagtc | tggggcagac | cttgtgcagc | caggggcctc | agtcaaggtg | 60 |
| tccctgcacag | cttctggctt | cgacattaag | gactactata | tacactggat | gaaacagagg | 120 |
| cctgaccagg | gcctggagtg | gatttggaaagg | gttgatcctg | acaatggtga | gactgaattt | 180 |
| gccccgaagt | tcccgggcaa | ggccactttt | acaacagaca | catcctccaa | cacagcctac | 240 |
| ctacaactca | gaggcctgac | atctgaggac | actgcccattct | attactgtgg | gagagaagac | 300 |
| tacgatggta | cctacacctg | gtttccttat | tggggccaag | ggactctgg | cactgtctct | 360 |
| gcagccaaaa | cgacacccccc | atctgtctat | ccactggccc | ctggatctgc | tgcccaaact | 420 |
| aactccatgg | tgaccctggg | atgcctggtc | aagggttatt | tccctgagcc | agtgacagtg | 480 |
| accttggaaact | ctggatccct | gtccagcgg | gtgcacacct | tcccagctgt | cctgcagtct | 540 |
| gacctctaca | ctctgagcag | ctcagtgact | gtcccttccaa | gcacctggcc | cagcgagacc | 600 |
| gtcacctgc | acgttgc | ccggcccage | agcaccaagg | tggacaagaa | aatttgtgccc | 660 |
| agggattgtg | gtttaagcc | ttgcataatgt | acagtcccaag | aagtatcatc | tgtcttcatc | 720 |
| ttccccccaa | agcccaagga | tgtgttcacc | attactctga | ctcctaaggt | cacgtgtgtt | 780 |
| gtggtagaca | tcaagcaagga | tgtatcccgag | gtccagttca | gttggtttgt | agatgtatgt | 840 |
| gaggtgcaca | cagctcagac | gcaaccccg | gaggagcgt | tcaacagcac | tttccgcctca | 900 |
| gtcagtgaac | ttccatcat | gcaccaggac | tggctcaatg | gcaaggagtt | caaatgcagg | 960 |
| gtcaacatgt | cagcttccc | tgc | gaaaaccca | tctccaaaac | caaaggcaga | 1020 |
| ccgaaggctc | cacaggtgt | caccattcca | cctccaaagg | agcagatggc | caaggataaa | 1080 |
| gtcagtctga | cctgcatgtat | aacagacttc | ttccctgtt | acattactgt | ggagtggcag | 1140 |
| tggatgggc | agccagcgg | gaactacaag | aacactcagc | ccatcatgg | cacagatggc | 1200 |
| tcttacttca | tctacagcaa | gctcaatgt | cagaagagca | actgggaggc | aggaaataact | 1260 |
| ttcacctgct | ctgtgttaca | tgagggcctg | cacaaccacc | atactgagaa | gagcctctcc | 1320 |
| cactctctg | gtaaatga | | | | | 1338 |

<210> SEQ ID NO 195

<211> LENGTH: 464

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 195

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Cys | Ser | Trp | Val | Ile | Phe | Phe | Leu | Met | Ala | Val | Val | Thr | Gly |
| 1 | | | | | 5 | | | 10 | | | | | | | 15 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Ser | Glu | Val | Gln | Leu | Gln | Gln | Ser | Gly | Ala | Asp | Leu | Val | Gln |
| | | | | 20 | | | 25 | | | | | | | | 30 |

-continued

Pro Gly Ala Ser Val Lys Val Ser Cys Thr Ala Ser Gly Phe Asp Ile
 35 40 45
 Lys Asp Tyr Tyr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu
 50 55 60
 Glu Trp Ile Gly Arg Val Asp Pro Asp Asn Gly Glu Thr Glu Phe Ala
 65 70 75 80
 Pro Lys Phe Pro Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn
 85 90 95
 Thr Ala Tyr Leu Gln Leu Arg Gly Leu Thr Ser Glu Asp Thr Ala Ile
 100 105 110
 Tyr Tyr Cys Gly Arg Glu Asp Tyr Asp Gly Thr Tyr Thr Trp Phe Pro
 115 120 125
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr
 130 135 140
 Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn
 145 150 155 160
 Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro
 165 170 175
 Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr
 180 185 190
 Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val
 195 200 205
 Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val
 210 215 220
 Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg
 225 230 235 240
 Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser
 245 250 255
 Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu
 260 265 270
 Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro
 275 280 285
 Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala
 290 295 300
 Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val
 305 310 315 320
 Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe
 325 330 335
 Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr
 340 345 350
 Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile
 355 360 365
 Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys
 370 375 380
 Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp
 385 390 395 400
 Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp
 405 410 415
 Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser
 420 425 430
 Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly
 435 440 445

-continued

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | His | Asn | His | His | Thr | Glu | Lys | Ser | Leu | Ser | His | Ser | Pro | Gly | Lys |
| 450 | | | | | | 455 | | | 460 | | | | | | |

<210> SEQ ID NO 196

<211> LENGTH: 1395

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 196

| | | | | | | |
|-------------|-------------|-------------|-------------|------------|------------|------|
| atgaaatgca | gctgggtcat | cttttcctg | atggcagtgg | ttacaggggt | caattcagaa | 60 |
| gttcagctgc | aacagtctgg | ggcagacatt | gtgcagccag | gggcctca | gttcaagggt | 120 |
| tgcacagctt | ctggcttcga | cattaaggac | tactatac | actggatgaa | acagaggcct | 180 |
| gaccagggcc | tggagtggat | tggaagggtt | gatcctgaca | atggtgagac | tgaatttgcc | 240 |
| cogaaggccc | cgggcaaggc | cacttttaca | acagacacat | cctccaacac | agcctaccta | 300 |
| caactcagag | gcctgacatc | tgaggacact | gccatctatt | actgtgggag | agaagactac | 360 |
| gatggtaacct | acacctggtt | tccttattgg | ggccaagggg | ctctggcac | tgtctctgca | 420 |
| gcacaaaacga | caccccccatt | tgtcttatcca | ctggccccctg | gatctgtgc | ccaaactaac | 480 |
| tccatggtga | ccctggatg | cctggtcaag | ggctatttcc | ctgagccagt | gacagtgacc | 540 |
| tggaactctg | gatccctgtc | cagcgggtgt | cacaccttc | cagctgtct | gcagttgtac | 600 |
| ctctacactc | tgagcagctc | agtgactgtc | ccctccagca | cctggccag | cgagaccgtc | 660 |
| acctgcaacg | ttgcccaccc | ggccagcagc | accaagggtgg | acaagaaaat | tgtgeccagg | 720 |
| gattgtgggt | gtaaggctt | catatgtaca | gtcccagaag | tatcatctgt | cttcatcttc | 780 |
| cccccaaagc | ccaaggatgt | gctaccatt | actctgactc | ctaaggcac | gtgtgttg | 840 |
| gttagacatca | gcaaggatga | tcccgaggtc | cagttcagct | ggtttgtaga | tgtgtggag | 900 |
| gtgcacacag | ctcagacgca | acccggggag | gagcagttca | acagcactt | ccgctcagtc | 960 |
| agtgaacttc | ccatcatgca | ccaggactgg | ctcaatggca | aggagttcaa | atgcagggtc | 1020 |
| aacagtgca | cttccctgc | ccccatcgag | aaaaccatct | ccaaaaccaa | aggcagaccg | 1080 |
| aaggctccac | aggtgtacac | cattccac | cccaaggagc | agatggccaa | ggataaagt | 1140 |
| agtctgaccc | gcatgataac | agacttcttc | cctgaagaca | ttactgtgga | gtggcagtg | 1200 |
| aatgggcagc | cagcggagaa | ctacaagaac | actcageccca | tcatggacac | agatggctct | 1260 |
| tacttcatct | acagcaagct | caatgtgcag | aagagcaact | gggaggcagg | aaatactt | 1320 |
| acctgctctg | tgttacatga | gggcctgcac | aaccaccata | ctgagaagag | cctctccac | 1380 |
| tctcctggta | aatga | | | | | 1395 |

<210> SEQ ID NO 197

<211> LENGTH: 214

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 197

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Leu | Gln | Met | Thr | Gln | Thr | Thr | Ser | Ser | Leu | Ser | Ala | Ser | Leu | Gly |
| 1 | | | | | | 5 | | | 10 | | | | 15 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Val | Thr | Ile | Ser | Cys | Arg | Ala | Ser | Gln | Asp | Ile | Ser | Asn | Tyr |
| | | | | | | | | | 25 | | | | | 30 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asn | Trp | Tyr | Gln | Gln | Lys | Pro | Asp | Gly | Thr | Val | Lys | Leu | Leu | Ile |
| | | | | | | 35 | | | 40 | | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Tyr | Thr | Ser | Thr | Leu | Gln | Ser | Gly | Val | Pro | Ser | Arg | Phe | Ser | Gly |
| | | | | | | 50 | | | 55 | | | 60 | | | |

US 9,089,553 B2

225**226**

-continued

Ser Gly Ser Gly Thr Asn Tyr Ser Leu Thr Ile Thr Asn Leu Glu Gln
65 70 75 80

Asp Asp Ala Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala
100 105 110

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
115 120 125

Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
130 135 140

Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
145 150 155 160

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
165 170 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
180 185 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
195 200 205

Phe Asn Arg Asn Glu Cys
210

<210> SEQ ID NO 198

<211> LENGTH: 645

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 198

gatctccaga tgacacagac tacttcctcc ctgtctgcct ctctggaga cagagtcacc 60
 atcaggta gggcaagtca ggacatttgc aattttttaa actggatataa gcagaaacca 120
 gatggaaactg ttaagtcctt gatcttctac acatcaacat tacagtcagg agtcccatcg 180
 aggttcagtg gcagtggttc tggaaacaaat tattctctca ccatttccaa cctggagcaa 240
 gatgatgctg ccacttactt ttgccaacag ggtgatacgc ttccgtacac gttcggaggg 300
 gggaccaagc tggaaataaa acgggctgtat gctgcaccaa ctgtatccat cttcccacca 360
 tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gtttttgaa caacttctac 420
 cccaaagaca tcaatgtcaa gtggaaagatt gatggcactg aacgacaaaa tggcgtcctg 480
 aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcact 540
 ttgaccaagg acgagttatga acgacataac agtataacct gtgaggccac tcacaagaca 600
 tcaacttcac ccattgtcaa gagcttcaac aggaatgagt gtttag 645

<210> SEQ ID NO 199

<211> LENGTH: 234

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 199

Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Leu Cys Phe Gln
1 5 10 15

Gly Ser Arg Cys Asp Leu Gln Met Thr Gln Thr Thr Ser Ser Leu Ser
20 25 30

Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp
35 40 45

Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val
50 55 60

-continued

Lys Leu Leu Ile Phe Tyr Thr Ser Thr Leu Gln Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Tyr Ser Leu Thr Ile Thr
85 90 95

Asn Leu Glu Gln Asp Asp Ala Ala Thr Tyr Phe Cys Gln Gln Gly Asp
100 105 110

Thr Leu Pro Tyr Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
130 135 140

Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
145 150 155 160

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
165 170 175

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
195 200 205

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
210 215 220

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225 230

<210> SEQ ID NO 200
<211> LENGTH: 705
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 200

| | |
|---|-----|
| atgatgtcct ctgctcagtt ccttggtctc ctgttgcct gtttcaagg ttccagatgt | 60 |
| gatctccaga tgacacagac tacttcctcc ctgtctgcct ctctgggaga cagagtccacc | 120 |
| atcagttgca gggcaagtca ggacattagc aattatttaa actggtatca gcagaaacca | 180 |
| gatggaaactg ttaagctcct gatcttctac acatcaacat tacagtccagg agtcccatcg | 240 |
| aggttcagtg gcagtgggtc tggAACAAAT tattctctca ccattaccaa cctggagcaa | 300 |
| gatgatgctg ccacttaactt ttgccaacag ggtgatacgc ttccgtacac gttcgaggg | 360 |
| gggaccaagc tggAAATAAA acgggctgat gctgcaccaa ctgtatccat cttcccacca | 420 |
| tccagtgagc agttaacatc tggaggtgcc tcagtcgtgt gtttcttcaa caacttctac | 480 |
| cccaaagaca tcaatgtcaa gtggaaagatt gatggcagtg aacgacaaaa tggcgtcctg | 540 |
| aacagttgga ctgatcagga cagcaaagac agcacctaca gcatgagcag caccctcacg | 600 |
| ttgaccaagg acgagtatga acgacataac agctataacct gtgaggccac tcacaagaca | 660 |
| tcaacttcac ccattgtcaa gagttcaac aggaatgagt gttag | 705 |

<210> SEQ ID NO 201
<211> LENGTH: 447
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 201

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

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Asn Met His Trp Met Lys Gln Asn Gln Gly Lys Ser Leu Glu Trp Ile
 35 40 45
 Gly Glu Ile Asn Pro Asn Ser Gly Gly Ser Gly Tyr Asn Gln Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Leu Gly Tyr Tyr Gly Asn Tyr Glu Asp Trp Tyr Phe Asp Val
 100 105 110
 Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Pro
 115 120 125
 Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
 130 135 140
 Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe
 165 170 175
 Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
 180 185 190
 Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
 195 200 205
 His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
 210 215 220
 Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val
 225 230 235 240
 Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr
 245 250 255
 Pro Lys Val Thr Cys Val Val Asp Ile Ser Lys Asp Asp Pro Glu
 260 265 270
 Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln
 275 280 285
 Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser
 290 295 300
 Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys
 305 310 315 320
 Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro
 340 345 350
 Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met
 355 360 365
 Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn
 370 375 380
 Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr
 385 390 395 400
 Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn
 405 410 415
 Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu
 420 425 430
 His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 435 440 445

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<210> SEQ ID NO 202
<211> LENGTH: 1344
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 202

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gaggtccagt tgcaacagt tggacctgaa ctaatgaagc ctggggcttc agtgaagatg      60
tcctgcaagg cttctggata cacattcaact gactacaaca tgcactggat gaagcagaac     120
caaggaaaga gcctagagt gataggagag attaatccta acagtggtgg ttctggttac     180
aaccagaagt tcaaaggcaa ggccacattt actgttagaca agtcctccag cacagcctac     240
atggagctcc gcagcctgac atctgaggac tctgcagtct attactgtgc aagattggc     300
tactatggta actacgagga ctggtattt gatgtctggg ggcgcaggagcac caccgttacc     360
gtctctctg caaaaacgac acccccacatct gtctatccac tggcccttgg atctgctgcc     420
caaactaact ccatggtgac cctgggatgc ctggtcaagg gctatttccc tgagccagtg     480
acagtgacct ggaactctgg atccctgtcc agcggtgtgc acacccccc agctgtctg     540
cagtcgtacc tctacactct gaggagctca gtgactgtcc cttccagcac ctggcccaagc     600
gagaccgtca cctgcaacgt tgcccacccg gccagcagca ccaagggtgga caagaaaatt     660
gtgcccaggg attgtggttt taaggcatttc atatgtacag tcccagaagt atcatctgtc     720
ttcatcttcc ccccaaagcc caaggatgtg ctcaccatta ctctgactcc taagggtcacc     780
tgtgttgtgg tagacatcag caaggatgtt cccgagggtt agttcagttt gttttagat     840
gatgtggagg tgcacacagc tcagacgca cccggggagg agcagttcaa cagcaacttc     900
cgctcagtca gtgaacttcc catcatgac caggactggc tcaatggcaa ggagttcaa     960
tgcagggtca acagtgcagc tttccctgtcc cccatcgaga aaaccatctc caaaaccaa     1020
ggcagaccga aggctccaca ggtgtacacc attccaccc ccaaggagca gatggccaag     1080
gataaaagtca gtctgacccctt catgataaca gacttcttcc ctgaagacat tactgtggag     1140
tggcagtgga atgggcagcc agcggagaac tacaagaaca ctcagcccat catggacaca     1200
gatggcttctt acttcatcta cagcaagtc aatgtgcaga agagcaactg ggaggcagga     1260
aataacttca cctgctctgt gttacatgag ggcctgcaca accaccatac tgagaagagc     1320
ctctccact ctccctggtaa atga                                         1344

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<210> SEQ ID NO 203
<211> LENGTH: 466
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 203

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Trp | Ser | Trp | Thr | Phe | Leu | Phe | Leu | Ser | Gly | Thr | Ser | Gly | |
| 1 | | | | | | | 5 | | 10 | | | 15 | | | |
| Val | Leu | Ser | Glu | Val | Gln | Leu | Gln | Gln | Ser | Gly | Pro | Glu | Leu | Met | Lys |
| | | | | 20 | | | | 25 | | | | | 30 | | |
| Pro | Gly | Ala | Ser | Val | Lys | Met | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe |
| | | | | 35 | | | 40 | | 45 | | | | | | |
| Thr | Asp | Tyr | Asn | Met | His | Trp | Met | Lys | Gln | Asn | Gln | Gly | Lys | Ser | Leu |
| | | | | 50 | | | 55 | | 60 | | | | | | |
| Glu | Trp | Ile | Gly | Glu | Ile | Asn | Pro | Asn | Ser | Gly | Gly | Ser | Gly | Tyr | Asn |
| | | | | 65 | | | 70 | | 75 | | | 80 | | | |
| Gln | Lys | Phe | Lys | Gly | Lys | Ala | Thr | Leu | Thr | Val | Asp | Lys | Ser | Ser | Ser |
| | | | | 85 | | | 90 | | 95 | | | | | | |

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Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Leu Gly Tyr Tyr Gly Asn Tyr Glu Asp Trp Tyr
 115 120 125
 Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys
 130 135 140
 Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln
 145 150 155 160
 Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro
 165 170 175
 Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val
 180 185 190
 His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser
 195 200 205
 Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys
 210 215 220
 Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val
 225 230 235 240
 Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val
 245 250 255
 Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile
 260 265 270
 Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp
 275 280 285
 Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His
 290 295 300
 Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
 305 310 315 320
 Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys
 325 330 335
 Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu
 340 345 350
 Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr
 355 360 365
 Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu
 370 375 380
 Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp
 385 390 395 400
 Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile
 405 410 415
 Met Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln
 420 425 430
 Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His
 435 440 445
 Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro
 450 455 460
 Gly Lys
 465

<210> SEQ ID NO 204
 <211> LENGTH: 1401
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus

-continued

<400> SEQUENCE: 204

| | |
|---|------|
| atgggatgga gctggacctt tctttcctc ctgtcaggaa cttcggtgt cctctctgag | 60 |
| gtccagttgc aacagtctgg acctgaacta atgaagctg gggcttcagt gaagatgtcc | 120 |
| tgcaaggctt ctggatacac attcaactgac tacaacatgc actggatgaa gcagaaccaa | 180 |
| gaaaagagcc tagagtggat aggagagatt aatcctaaca gtgggttgtc tggttacaac | 240 |
| cagaagttca aaggcaaggc cacattgact gtagacaagt cttccagcac agcctacatg | 300 |
| gagctccgca gcctgacatc tgaggactct gcagtttattt actgtgcaag attgggctac | 360 |
| tatggtaact acgaggactg gtatttcgtat gtctggggcg cagggaccac ggtcaccgtc | 420 |
| tcctctgcca aaacgacacc cccatctgtc tatccactgg cccctggatc tgctgccaa | 480 |
| actaactcca tggtgaccct gggatgcctg gtcaaggctt atttccctga gccagtgaca | 540 |
| gtgacctgga actctggatc cctgtccagc ggtgtgcaca cttcccagc tgctctgcag | 600 |
| tctgacccctt acactctgag cagtcagtg actgtccccctt ccagcacctg gcccagcag | 660 |
| acccgtcacctt gcaacgttgc ccacccggcc agcagcacca aggtggacaa gaaaatttg | 720 |
| cccgaggattt gtgggtgtaa gccttgcata tgtacagtcc cagaagtatc atctgtttc | 780 |
| atcttccccca caaagcccaa ggtatgtgctc accattactc tgactcttaa ggtcacgtgt | 840 |
| gttgggttag acatcagcaa ggtatgtccc gaggtccagt tcagctggtt tggatgtat | 900 |
| gtggagggtgc acacagctca gacgcaaccc cgggaggagc agttcaacag cactttccgc | 960 |
| tcagtcagtg aacttcccat catgcaccag gactggctca atggcaagga gttcaaatgc | 1020 |
| aggggtcaaca gtgcagcttt ccctgcccccc atcgagaaaa ccatttccaa aaccaaggc | 1080 |
| agaccgaagg ctccacaggt gtacaccattt ccaccccttccaa aggagcagat ggccaaggat | 1140 |
| aaagtcaatc tgacctgcat gataacagac ttcttccctg aagacattac tggggatgg | 1200 |
| cagtgaaatg ggcagccagc ggagaactac aagaacactc agcccatcat ggacacagat | 1260 |
| ggctttaactt tcatctacag caagctcaat gtgcagaaga gcaactggga ggcaggaaat | 1320 |
| actttcacctt gctctgtttt acatgaggccc ctgcacaacc accataactga gaagagcctc | 1380 |
| tcccaactctc ctggtaatg a | 1401 |

<210> SEQ_ID NO 205

<211> LENGTH: 215

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 205

| | |
|---|--|
| Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly | |
| 1 5 10 15 | |

| | |
|---|--|
| Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Thr Ser Ser | |
| 20 25 30 | |

| | |
|---|--|
| Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Leu Trp | |
| 35 40 45 | |

| | |
|---|--|
| Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser | |
| 50 55 60 | |

| | |
|---|--|
| Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Val Glu | |
| 65 70 75 80 | |

| | |
|---|--|
| Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Phe Phe Pro | |
| 85 90 95 | |

| | |
|---|--|
| Ser Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala | |
| 100 105 110 | |

-continued

Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser
115 120 125

Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp
130 135 140

Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val
145 150 155 160

Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met
165 170 175

Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser
180 185 190

Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys
195 200 205

Ser Phe Asn Arg Asn Glu Cys
210 215

<210> SEQ ID NO 206
<211> LENGTH: 645
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 206

cagattgttc tcacccagtc tccagcaatc atgtctgcat ctccaggggga gaaggtcacc 60
atgacctgca gggccagctc aagtgttaact tccagttact tgaactggta ccagcagaag 120
ccaggatctt cccccaaact ctggatttat agcacatcca acctggcttc aggagtccca 180
gtcgcttca gtggcagtgg gtcgtggacc tcttactctc tcacaatcag cagtgtggag 240
gtcgaggatg ctgccactta ttactgccag cagtagtattt ttttccatc gacgttcggt 300
ggaggccacca agctggaaat caagcgggct gatgctgcac caactgtata catttccca 360
ccatccagtg agcagttAAC atctggaggt gcctcagtcg tgtgcttctt gaacaacttc 420
taccccaaAG acatcaatgt caagtggaaAG attgatggca gtgaacgcaca aaatggcgTC 480
ctgaacagtt ggactgtatca ggacagcaAA gacagccACT acagcatgAG cagcaccCTC 540
acgttgacca aggacgagta tgaacgcAC aacagctata cctgtgaggc cactcacaAG 600
acatcaactt cacccatcgt caagagcttc aacaggaatg agtgt 645

<210> SEQ ID NO 207
<211> LENGTH: 237
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 207

Met Asp Ser Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Leu
1 5 10 15

Val Lys Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
20 25 30

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45

Ser Ser Val Thr Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Ser Ser Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly
65 70 75 80

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
85 90 95

Thr Ile Ser Ser Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
100 105 110

US 9,089,553 B2

239**240**

-continued

Gln Tyr Asp Phe Phe Pro Ser Thr Phe Gly Gly Gly Thr Lys Leu Glu
 115 120 125

Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser
 130 135 140

Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn
 145 150 155 160

Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser
 165 170 175

Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys
 180 185 190

Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu
 195 200 205

Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser
 210 215 220

Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 225 230 235

<210> SEQ ID NO 208

<211> LENGTH: 711

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 208

atggattctc aagtgcagat tttcagcttc cttctaataca gtgccttagt caaaaatgtcc 60
 agaggacaga ttgttctcac ccagtctcca gcaatcatgt ctgcacatctcc aggggagaag 120
 gtcaccatga cctgcagggc cagtcatagt gtaacttcca gttacttgaa ctggtaccag 180
 cagaaggccag gatcttcccc caaactctgg atttatacgca catccaaacct ggcttcagga 240
 gtcccaagctc gcttcagtg 240 cagtggtctt gggacctctt actctctcac aatcagcagt 300
 gtggaggctg agatgtctgc cacttattac tgccagcagt atgattttt cccatcgacg 360
 ttccggggag gcaccaagct gaaaaatcaag cgggctgtatcgatc ctgcaccaac tttatccatc 420
 ttcccacccat ccagtgcgc 420 gttaacatct ggaggtgcct cagtcgtgtg cttcttgcac 480
 aacttctacc ccaaagacat caatgtcaag tggaaagattt atggcagtga acgacaataat 540
 ggctgttgc 540 acagttggac tgatcaggac agcaaaagaca gcacccatcag catgagcagc 600
 accctcacgt tgaccaagga cgagttatgaa cgacataaca gctataccctg tgaggccact 660
 cacaagacat caacttcacc catcgtaag agcttcaaca ggaatgagtg t 711

<210> SEQ ID NO 209

<211> LENGTH: 445

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 209

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Tyr Met Asn Trp Val Lys Gln Ser His Gly Glu Ser Leu Glu Trp Ile
 35 40 45

Gly Asp Ile Asn Pro Tyr Asn Asp Asp Thr Thr Tyr Asn His Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr
 65 70 75 80

-continued

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Glu Thr Ala Val Ile Thr Thr Asn Ala Met Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser
 115 120 125
 Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val
 130 135 140
 Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro
 180 185 190
 Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro
 195 200 205
 Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
 210 215 220
 Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile
 225 230 235 240
 Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys
 245 250 255
 Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln
 260 265 270
 Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln
 275 280 285
 Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu
 290 295 300
 Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg
 305 310 315 320
 Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 325 330 335
 Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro
 340 345 350
 Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr
 355 360 365
 Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
 370 375 380
 Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly
 385 390 395 400
 Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu
 405 410 415
 Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn
 420 425 430
 His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 435 440 445

<210> SEQ_ID NO 210

<211> LENGTH: 1335

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 210

gagggtccagc tgcaacaatc tggacctgag ctgggtgaagc ctggggcttc agtgaagatg

60

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| | | | | | | |
|--------------|------------|-------------|-------------|-------------|-------------|------|
| tcctgtttaagg | tttctggata | cacattcaact | gactactaca | tgaactgggt | gaagcagagc | 120 |
| catggagaga | gccttgagtg | gattggagat | attaatcctt | acaacgtatga | tactacctac | 180 |
| aaccacaagt | tcaagggcaa | ggccacattg | actgttagaca | aatcctccaa | cacagcctac | 240 |
| atgcagctca | acagcctgac | atctgaggac | tctgcagtct | attactgtgc | aagagagacg | 300 |
| gccgttatta | ctacgaatgc | tatggactac | tggggtcaag | gaacctca | gaccgtctcc | 360 |
| tca | cgccaaaa | cgacaccccc | atctgtctat | ccactggccc | ctggatctgc | 420 |
| aactccatgg | tgaccctggg | atgcctggtc | aagggttatt | tccctgagcc | agtgacagt | 480 |
| acctggaact | ctggatccct | gtccagcgg | gtgcacac | tccctgatgt | cctgcagtct | 540 |
| gacctctaca | ctctgagcag | ctcagtgact | gtccccctcca | gcacctggcc | cagcgagacc | 600 |
| gtcacccgtca | acgttgc | cccgccccc | agcaccaagg | tggacaagaa | aatttgtgccc | 660 |
| agggattgtg | gttgttgc | ttgcataatgt | acagttccag | aagtatcatc | tgtcttcatc | 720 |
| ttccccccaa | agcccaagga | tgtgttcacc | attactctga | ctcctaaggt | cacgtgtt | 780 |
| gtggtagaca | ttagcaagga | tgtatcccag | gtccagttca | gtgggttgt | agatgtatgt | 840 |
| gaggtgcaca | cagtcagac | gcaacccccc | gaggagcgt | tcaacagcac | tttccgcgtca | 900 |
| gtcagtgAAC | ttccatcat | gcaccaggac | tggctcaatg | gcaaggagtt | caaatgcagg | 960 |
| gtcaacagt | cagcttccc | tgccccatc | gagaaaacc | tctccaaac | caaaggcaga | 1020 |
| cggaggc | cacaggtgt | caccattcca | cctcccaagg | agcagatggc | caaggataaa | 1080 |
| gtcagtgat | cctgtatgt | aacagacttc | ttccctgaa | acattactgt | ggagtggcag | 1140 |
| tggaaatggc | agccagcgg | gaactacaag | aacactcagc | ccatcatgga | cacagatggc | 1200 |
| tcttacttca | tctacagcaa | gctcaatgt | cagaagagca | actggggaggc | aggaaataact | 1260 |
| ttcacctgct | ctgtgttaca | tgagggcctg | cacaaccacc | atactgagaa | gagcctctcc | 1320 |
| cactctctg | gtaaaa | | | | | 1335 |

<210> SEQ ID NO 211

<211> LENGTH: 464

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 211

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Trp | Asn | Trp | Ile | Phe | Leu | Phe | Leu | Leu | Ser | Gly | Thr | Ala | Gly |
| 1 | | | | | 5 | | | | 10 | | | | 15 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Ser | Glu | Val | Gln | Leu | Gln | Gln | Ser | Gly | Pro | Glu | Leu | Val | Lys |
| | | | | 20 | | | | 25 | | | | 30 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Ala | Ser | Val | Lys | Met | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Thr | Phe |
| | | | | 35 | | | | 40 | | | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asp | Tyr | Tyr | Met | Asn | Trp | Val | Lys | Gln | Ser | His | Gly | Glu | Ser | Leu |
| | | | | 50 | | | | 55 | | | 60 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Trp | Ile | Gly | Asp | Ile | Asn | Pro | Tyr | Asn | Asp | Asp | Thr | Thr | Tyr | Asn |
| 65 | | | | | 70 | | | | 75 | | | 80 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Lys | Phe | Lys | Gly | Lys | Ala | Thr | Leu | Thr | Val | Asp | Lys | Ser | Ser | Asn |
| | | | | | 85 | | | | 90 | | | 95 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Tyr | Met | Gln | Leu | Asn | Ser | Leu | Thr | Ser | Glu | Asp | Ser | Ala | Val |
| | | | | 100 | | | | 105 | | | 110 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Cys | Ala | Arg | Glu | Thr | Ala | Val | Ile | Thr | Thr | Asn | Ala | Met | Asp |
| | | | | 115 | | | | 120 | | | 125 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Trp | Gly | Gln | Gly | Thr | Ser | Val | Thr | Val | Ser | Ser | Ala | Lys | Thr | Thr |
| | | | | | 130 | | | 135 | | | 140 | | | | |

-continued

Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn
 145 150 155 160
 Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro
 165 170 175
 Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr
 180 185 190
 Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val
 195 200 205
 Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val
 210 215 220
 Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg
 225 230 235 240
 Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser
 245 250 255
 Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu
 260 265 270
 Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro
 275 280 285
 Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala
 290 295 300
 Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val
 305 310 315 320
 Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe
 325 330 335
 Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr
 340 345 350
 Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile
 355 360 365
 Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys
 370 375 380
 Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp
 385 390 395 400
 Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp
 405 410 415
 Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser
 420 425 430
 Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly
 435 440 445
 Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 450 455 460

<210> SEQ_ID NO 212
 <211> LENGTH: 1392
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 212

```

atgggatgga actggatctt tcttttcctc ttgtcaggaa ctgcaggtgt ctactctgag      60
gtccagctgc aacaatctgg acctgagctg gtgaagcctg gggcttcagt gaagatgtcc     120
tgtaaggctt ctggatacac attcaactgac tactacatga actgggtgaa gcagagccat     180
ggagagagcc ttgagtggat tggagatatt aatccttaca acgatgatac tacctacaac     240
cacaagttca agggcaaggc cacattgact gtagacaaat cctccaacac agcctacatg     300
  
```

-continued

| | |
|---|------|
| cagctcaaca gcctgacatc tgaggactct gcagtctatt actgtgcagg agagacggcc | 360 |
| gttattacta cgaatgctat ggactactgg ggtcaaggaa cctcagtcac cgtctccctca | 420 |
| gccaaacga cacccccatc tgtctatcca ctggccctg gatctgctgc ccaaactaac | 480 |
| tccatggta ccctggatg cctggtaag ggctattcc ctgagccagt gacagtgacc | 540 |
| tggaaactctg gatccctgtc cagcggtgtg cacacccatc cagctgtctc gcagtctgac | 600 |
| ctctacatc tgagcagctc agtgcactgtc cctccagca cctggccag cgagaccgtc | 660 |
| acctgcaacg ttgcccaccc ggccagcagc accaagggtgg acaagaaaat tgtgccagg | 720 |
| gattgtgggt gtaagcctt catatgtaca gtcccagaag tatcatctgt cttcatctc | 780 |
| cccccaaagc ccaaggatgt gtcaccatt actctgactc ctaaggtcac gtgtgttgt | 840 |
| gttagacatca gcaaggatga tcccgaggtc cagttcagtc ggtttgtaga ttagtgtggag | 900 |
| gtgcacacag ctcagacgca accccggag gaggcgttca acagcactt ccgctcagtc | 960 |
| agtgaacttc ccatcatgca ccaggactgg ctcaatggca aggagttcaa atgcagggtc | 1020 |
| aacagtgcag cttccctgc cccatcgag aaaaccatct caaaaaccaa aggccagaccg | 1080 |
| aaggctccac aggtgtacac cattccaccc cccaggcagc agatggccaa ggataaaagtc | 1140 |
| agtctgacct gcatgataac agacttcttc cctgaagaca ttactgtgga gtggcagtgg | 1200 |
| aatgggcagc cagcggagaa ctacaagaac actcagccca tcatggacac agatggctct | 1260 |
| tacttcatct acagcaagct caatgtgcag aagagcaact gggaggcagg aaatactttc | 1320 |
| acctgctctg tgttacatga gggcctgcac aaccaccata ctgagaagag cctctccac | 1380 |
| tctcctggta aa | 1392 |

<210> SEQ_ID NO 213

<211> LENGTH: 215

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 213

| | | | |
|---|---|----|----|
| Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly | | | |
| 1 | 5 | 10 | 15 |

| | | | |
|---|----|----|--|
| Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Val Thr Ser Ser | | | |
| 20 | 25 | 30 | |

| | | | |
|---|----|----|--|
| Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu | | | |
| 35 | 40 | 45 | |

| | | | |
|---|----|----|--|
| Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser | | | |
| 50 | 55 | 60 | |

| | | | |
|---|----|----|----|
| Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln | | | |
| 65 | 70 | 75 | 80 |

| | | | |
|---|----|----|--|
| Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Phe Phe Pro | | | |
| 85 | 90 | 95 | |

| | | | |
|---|-----|-----|--|
| Ser Thr Phe Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala | | | |
| 100 | 105 | 110 | |

| | | | |
|---|-----|-----|--|
| Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser | | | |
| 115 | 120 | 125 | |

| | | | |
|---|-----|-----|--|
| Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu | | | |
| 130 | 135 | 140 | |

| | |
|---|--|
| Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser | |
|---|--|

-continued

| | | | |
|---|-----|-----|-----|
| 145 | 150 | 155 | 160 |
| Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu | | | |
| | 165 | 170 | 175 |
| Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val | | | |
| | 180 | 185 | 190 |
| Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys | | | |
| | 195 | 200 | 205 |
| Ser Phe Asn Arg Gly Glu Cys | | | |
| | 210 | 215 | |

```
<210> SEQ ID NO 214
<211> LENGTH: 645
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody Sequence
```

```
<210> SEQ ID NO 215
<211> LENGTH: 237
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence
```

<400> SEQUENCE: 215
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp

1 5 10 15
Leu Pro Gly Ala Arg Cys Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser

Ser Ser Val Thr Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
50 55 60

Lys Ala Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly
65 70 75 80

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu
85 90 95

-continued

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
 100 105 110
 Gln Tyr Asp Phe Phe Pro Ser Thr Phe Gly Gly Thr Lys Val Glu
 115 120 125
 Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
 130 135 140
 Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
 145 150 155 160
 Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
 165 170 175
 Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
 180 185 190
 Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
 195 200 205
 Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
 210 215 220
 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> SEQ_ID NO 216
 <211> LENGTH: 711
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Polynucleotide
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 216

| | | | | | | |
|------------|------------|------------|-------------|-------------|-------------|-----|
| atggacatga | gggtccccgc | tcagctctg | gggctctgc | tactctggct | cccgagggcc | 60 |
| agatgtgaca | tccagctgac | ccagagcccc | agttccctt | ccgcattccgt | tggtgaccga | 120 |
| gttacaatca | catgcccgc | ctcatcttca | gttacatct | tttatcttaa | ttggtatcaa | 180 |
| caaaaaccag | aaaaagcacc | taaacttctt | atatactcta | catctaattct | cgcattcagga | 240 |
| gttccctctc | gatttcagg | atctggatca | ggcacagaat | ttacacttac | tatatcatca | 300 |
| ctccaaccag | aagacttcgc | cacttattac | tgccaacaat | acgattttt | tccaaggcaca | 360 |
| ttcggaggag | gtacaaaagt | agaaatcaag | cgtacggtgg | ctgcaccatc | tgtcttcatc | 420 |
| ttcccgccat | ctgatgagca | gttgaatct | ggaactgccc | ctgttgtgt | cctgctgaat | 480 |
| aacttctatc | ccagagaggc | caaagtacag | tggaagggtgg | ataacgcct | ccaatcggt | 540 |
| aactcccagg | agagtgtcac | agagcaggac | agcaaggaca | gcacctacag | cctcagcagc | 600 |
| accctgacgc | tgagcaaagc | agactacgag | aaacacaaag | tctacgcctg | cgaagtcacc | 660 |
| catcagggcc | tgagctcgcc | cgtcacaaag | agcttcaaca | ggggagagtg | t | 711 |

<210> SEQ_ID NO 217
 <211> LENGTH: 447
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Polypeptide
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 217

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

-continued

| 1 | 5 | 10 | 15 |
|---|-----|-----|-----|
| Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr | | | |
| 20 | 25 | 30 | |
| Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met | | | |
| 35 | 40 | 45 | |
| Gly Asp Ile Asn Pro Tyr Asn Asp Asp Thr Thr Tyr Asn His Lys Phe | | | |
| 50 | 55 | 60 | |
| Lys Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr | | | |
| 65 | 70 | 75 | 80 |
| Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys | | | |
| 85 | 90 | 95 | |
| Ala Arg Glu Thr Ala Val Ile Thr Thr Asn Ala Met Asp Tyr Trp Gly | | | |
| 100 | 105 | 110 | |
| Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser | | | |
| 115 | 120 | 125 | |
| Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala | | | |
| 130 | 135 | 140 | |
| Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val | | | |
| 145 | 150 | 155 | 160 |
| Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala | | | |
| 165 | 170 | 175 | |
| Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val | | | |
| 180 | 185 | 190 | |
| Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His | | | |
| 195 | 200 | 205 | |
| Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys | | | |
| 210 | 215 | 220 | |
| Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val | | | |
| 225 | 230 | 235 | 240 |
| Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr | | | |
| 245 | 250 | 255 | |
| Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp Pro Glu | | | |
| 260 | 265 | 270 | |
| Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys | | | |
| 275 | 280 | 285 | |
| Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser | | | |
| 290 | 295 | 300 | |
| Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys | | | |
| 305 | 310 | 315 | 320 |
| Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile | | | |
| 325 | 330 | 335 | |
| Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro | | | |
| 340 | 345 | 350 | |
| Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu | | | |
| 355 | 360 | 365 | |
| Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn | | | |
| 370 | 375 | 380 | |
| Gly Gln Pro Glu Asn Asn Tyr Lys Thr Pro Pro Met Leu Asp Ser | | | |
| 385 | 390 | 395 | 400 |
| Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg | | | |
| 405 | 410 | 415 | |
| Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu | | | |
| 420 | 425 | 430 | |

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| His | Asn | His | Tyr | Thr | Gln | Lys | Ser | Leu | Ser | Leu | Ser | Pro | Gly | Lys | | |
| | | | | | | | 435 | | | | | 440 | | | | 445 |

```
<210> SEQ ID NO 219
<211> LENGTH: 466
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence
```

<400> SEQUENCE: 219
Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly

-continued

Ala His Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Asp Tyr Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Arg Leu
 50 55 60

Glu Trp Met Gly Asp Ile Asn Pro Tyr Asn Asp Asp Thr Thr Tyr Asn
 65 70 75 80

His Lys Phe Lys Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser
 85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Glu Thr Ala Val Ile Thr Thr Asn Ala Met Asp
 115 120 125

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
 130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
 145 150 155 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
 180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 195 200 205

Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn
 210 215 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg
 225 230 235 240

Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
 245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 275 280 285

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 290 295 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
 305 310 315 320

Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys
 325 330 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu
 340 345 350

Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 355 360 365

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 385 390 395 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met
 405 410 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 420 425 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His

US 9,089,553 B2

259**260**

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435 440 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 450 455 460

Gly Lys
 465

<210> SEQ ID NO 220
<211> LENGTH: 1398
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 220

| | | | | | | |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| atggactgga | cctggaggat | cctttcttg | gtggcagcag | ccacaggagc | ccactccgag | 60 |
| gtgcagctgg | tgcagagcgg | cgcgcaggtc | aagaaacctg | gagcaagcgt | aaaggtagt | 120 |
| tgcaaagcat | ctggatacac | atttaccgac | tactacatga | attgggtacg | acaagcccct | 180 |
| ggacaaaagac | ttgaatggat | gggagacatt | aacccttata | acgacgacac | tacataacaat | 240 |
| cataaaattta | aaggaagagt | tacaattaca | agagatacat | cogcatcaac | cgcctatatg | 300 |
| gaactttctt | catttagatc | tgaagacact | gctgtttatt | actgtgcaag | agaaaactgcc | 360 |
| gttattacta | ctaaccgtat | ggattactgg | ggtcaaggaa | ccactgttac | cgtctctagt | 420 |
| gcctccacca | agggeccatc | ggttttcccc | ctggcgccct | gctccaggag | caccccgag | 480 |
| agcacacgccc | ccctgggctg | cctggtcaag | gactacttcc | ccgaaccggt | gacggtgtcg | 540 |
| tggaacttcag | gcgcctctgac | cageggcggt | cacacccctc | cagctgtcct | acagtccctca | 600 |
| ggactctact | ccctcagcag | cgtggtgacc | gtgccttcca | gcaacttcgg | cacccagacc | 660 |
| tacacccgtca | acgttagatca | caagcccagc | aacaccaagg | tggacaagac | agttgagcgc | 720 |
| aatgttgtg | tcgagtgccc | accgtgccc | gcaccacctg | tggcaggacc | gtcagtcttc | 780 |
| ctcttcccc | aaaaacccaa | ggacacccctc | atgatctccc | ggacccctga | ggtcacgtgc | 840 |
| gtgggtgtgg | acgtgagcca | cgaagacccc | gaggtccagt | tcaactggta | cgtggacggc | 900 |
| gtggaggatgc | ataatgccaa | gacaaagcca | cgggaggagc | agttcaacag | cacgtccgt | 960 |
| gtgggtcagcg | tcctcaccgt | tgtgcaccag | gactggctga | acggcaagga | gtacaagtgc | 1020 |
| aagggtctcca | acaaaggccct | cccaagcccc | atcgagaaaa | ccatctccaa | aaccaaagg | 1080 |
| cagccccgag | aaccacaggt | gtacacccctg | cccccatccc | gggaggagat | gaccaagaac | 1140 |
| caggtcagcc | tgacccgtct | ggtcaaaaggc | ttctacccca | gacgacatcgc | cgtggagtg | 1200 |
| gagagcaatg | ggcagccgga | gaacaactac | aagaccacac | ctcccatgct | ggactccgac | 1260 |
| ggctcttct | tcctctacag | caagctcacc | gtggacaaga | gcaggtggca | gcaggggaac | 1320 |
| gtcttctcat | gtcccggtat | gcatgaggct | ctgcacaacc | actacacgca | gaagagcctc | 1380 |
| tccctgtctc | cgggtaaa | | | | | 1398 |

<210> SEQ ID NO 221
<211> LENGTH: 215
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence

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<400> SEQUENCE: 221
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Val Ser Ser Thr Ile Ser Ser Asn
 20 25 30
 His Leu His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu
 35 40 45
 Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser
 50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
 65 70 75 80
 Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro
 85 90 95
 Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
 100 105 110
 Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125
 Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140
 Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160
 Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175
 Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 180 185 190
 Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 195 200 205
 Ser Phe Asn Arg Gly Glu Cys
 210 215

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<210> SEQ ID NO 222
<211> LENGTH: 645
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody Sequence
```

<400> SEQUENCE: 222
gacatccaga tgaccaggc tccatccctcc ctctcagcat ccgttaggcga tagagttaca 60
ataaacatgca gcgttatcatc aactatatca tcaaattatc ttcatgggtt ccaacagaaa 120
cccgccaag cacctaaatc acttatatac ggcacatcaa atctcgcatc aggcgttcct 180
tcaagattt caggctctgg ctcaggcacc gactttactc ttacaatatc ctcccccaa 240
cccgaaagact tcgcaacccta ttactgtcaa caatggtctt catatccact cacatttgc 300
ggcgccacaa aagttagaaat taaacgtacg gtggctgcac catctgtctt catctcccg 360
ccatctgtatc agcagttgaa atcttggact gcctctgttg tgtgcctgct gaataacttc 420
tatcccagag aggccaaagt acagtggaaag gtggataacg ccctccaatc gggtaactcc 480
caggagatgt tcacagagca ggacagcaag gagacacct acagcctcag cagcacccctg 540
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcatc 600
ggcctqaqct cqcccccac aaaaqqcttc aacaqqqqqaq aqtq 645

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<210> SEQ ID NO 223
<211> LENGTH: 237
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 223

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Val Ser
35 40 45

Ser Thr Ile Ser Ser Asn His Leu His Trp Phe Gln Gln Lys Pro Gly
50 55 60

Lys Ala Pro Lys Ser Leu Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly
65 70 75 80

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
85 90 95

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
100 105 110

Gln Trp Ser Ser Tyr Pro Leu Thr Phe Gly Gly Thr Lys Val Glu
115 120 125

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145 150 155 160

Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
165 170 175

Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
180 185 190

Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
195 200 205

Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
210 215 220

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

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<210> SEQ ID NO 224
<211> LENGTH: 711
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 224

atggacatga gggccccgc tcagtcctg gggctcctgc tactctggct ccgagggtgcc      60
agatgtgaca tccatgtac ccagtctcca tctccctct cagcatccgt aggcgataga     120
gttacaataa catgcagcgt atcatcaact atatcatcaa atcatttca ttggttccaa     180
cagaaaccgc ccaaaggcacc taaatcactt atataccggc catcaaatct cgcgcattggc      240
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gttcctcaa gatttcagg ctctggctca ggcaccgact ttactttac aatatccctcc      300
ctccaaacctcg aagacttcgc aacctattac tgtcaacaat ggctctata tccactcaca      360
tttggggcg gcacaaaaagt agaaataaa cgtacggtgg ctgcaccatc tgtttcatc      420
ttccccat ctgatgagca gttgaatct ggaactgcct ctgttgttg cctgctgaat      480
aacttctatc ccagagaggc caaagtacag tggaaagggtgg ataacgcct ccaatcggt      540
aactcccagg agagtgcac agaggcaggc agcaaggaca gcacctacag cctcagcagc      600
accctgacgc tgagcaaagc agactacag aaacacaaag tctacgcctg cgaagtcacc      660
catcagggcc tgagtcgcc cgtaaaaaaagc agttcaaca ggggagagtg t      711

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<210> SEQ_ID NO 225
<211> LENGTH: 451
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 225

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Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1           5          10          15

Ser Val Lys Val Ser Cys Lys Ala Ser Asp Phe Asn Ile Lys Asp Phe
20          25          30

Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35          40          45

Gly Arg Ile Asp Pro Glu Asn Gly Asp Thr Leu Tyr Asp Pro Lys Phe
50          55          60

Gln Asp Lys Val Thr Met Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65          70          75          80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85          90          95

Ala Arg Glu Ala Asp Tyr Phe His Asp Gly Thr Ser Tyr Trp Tyr Phe
100         105         110

Asp Val Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115         120         125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
130         135         140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145         150         155         160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
165         170         175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
180         185         190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
195         200         205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
210         215         220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225         230         235         240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245         250         255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

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US 9,089,553 B2

267**268**

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| 260 | 265 | 270 |
|---|-----|-----|
| Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val | | |
| 275 | 280 | 285 |
| His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe | | |
| 290 | 295 | 300 |
| Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly | | |
| 305 | 310 | 315 |
| Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile | | |
| 325 | 330 | 335 |
| Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val | | |
| 340 | 345 | 350 |
| Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser | | |
| 355 | 360 | 365 |
| Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu | | |
| 370 | 375 | 380 |
| Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro | | |
| 385 | 390 | 395 |
| Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val | | |
| 405 | 410 | 415 |
| Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met | | |
| 420 | 425 | 430 |
| His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser | | |
| 435 | 440 | 445 |
| Pro Gly Lys | | |
| 450 | | |

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<210> SEQ_ID NO 226
<211> LENGTH: 1353
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 226

gaggtgcagc tggtgcaagtc tggggctgag gtgaagaagc ctggggccctc agtgaaggc 60
tcctgcaagg cttctgactt caacattaaa gacttctatc tacactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatttggaaagg attgatcctg agaatggta tactttatat 180
gaccgcagaat tccaggacaa ggtcaccatg accacagaca cgtccaccag cacagctac 240
atggagactga ggagccctgag atctgacgc acggccgtgt attactgtgc gagagaggcg 300
gattatttcc acgtatggta ctcctactgg tacttcgtatg tctggggccg tggcacctg 360
gtcaccgtct ctatgtccctc caccaaggcc ccatcggtct tccccctggc gcccgtctcc 420
aggagcacct ccgagagcac acggccctg ggctgcctgg tcaaggacta cttccccgaa 480
ccgggtgacgg tgcgtggaa ctcaggccgt ctgaccagcg gctgcacac cttcccaagct 540
gtcctacagt ctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcaac 600
ttcggccaccc agacctacac ctgcaacgta gatcacaagc ccagcaacac caaggtggac 660
aagacagttg agcgcaaatg ttgtgtcgag tgcccaccgt gcccagcacc acctgtggca 720
ggaccgtcag tcttcctt cccccaaaaa cccaaggaca ccctcatgtat ctccggacc 780
cctgaggatca cgtgegtgggt ggtggacgtg agccacgaa accccgaggt ccagttaac 840
tggtaacgtgg acggcgtggaa ggtgcataat gccaagacaa agccacggaa ggacgttc 900
aacagcacgt tccgtgtggt cagcgtccctc accgttgtgc accaggactg gctgaacggc 960

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| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| aaggagtaca | agtgcaggt | ctccaacaaa | ggcctccag | ccccatcga | gaaaaccatc | 1020 |
| tccaaaacca | aaggcagcc | ccgagaacca | caggtgtaca | ccctgcccc | atccgggag | 1080 |
| gagatgacca | agaaccagg | cagcctgacc | tgcctggta | aaggcttcta | ccccagcgac | 1140 |
| atcgccgtgg | agtgggagag | caatgggcag | ccggagaaca | actacaagac | cacacccc | 1200 |
| atgctggact | ccgacggctc | cttcttcctc | tacagcaagc | tcaccgtgga | caagagcagg | 1260 |
| tggcagcagg | ggaacgtctt | ctcatgctcc | gtatgcatg | aggctctgca | caaccactac | 1320 |
| acgcagaaga | gccttcctc | gttccgggt | aaa | | | 1353 |

<210> SEQ ID NO 227
<211> LENGTH: 470
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 227

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Trp | Thr | Trp | Arg | Ile | Leu | Phe | Leu | Val | Ala | Ala | Ala | Thr | Gly |
| 1 | | | | | | 5 | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | His | Ser | Glu | Val | Gln | Leu | Val | Gln | Ser | Gly | Ala | Glu | Val | Lys | Lys |
| | | | 20 | | | | | 25 | | | | 30 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Ala | Ser | Val | Lys | Val | Ser | Cys | Lys | Ala | Ser | Asp | Phe | Asn | Ile |
| | 35 | | | | | 40 | | | | | 45 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asp | Phe | Tyr | Leu | His | Trp | Val | Arg | Gln | Ala | Pro | Gly | Gln | Gly | Leu |
| | 50 | | | | | 55 | | | 60 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Trp | Ile | Gly | Arg | Ile | Asp | Pro | Glu | Asn | Gly | Asp | Thr | Leu | Tyr | Asp |
| | 65 | | | | | 70 | | | 75 | | | 80 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Lys | Phe | Gln | Asp | Lys | Val | Thr | Met | Thr | Thr | Asp | Thr | Ser | Thr | Ser |
| | 85 | | | | | 90 | | 95 | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Tyr | Met | Glu | Leu | Arg | Ser | Leu | Arg | Ser | Asp | Asp | Thr | Ala | Val |
| | 100 | | | | | 105 | | | | 110 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Cys | Ala | Arg | Glu | Ala | Asp | Tyr | Phe | His | Asp | Gly | Thr | Ser | Tyr |
| | 115 | | | | | 120 | | | 125 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Tyr | Phe | Asp | Val | Trp | Gly | Arg | Gly | Thr | Leu | Val | Thr | Val | Ser | Ser |
| | 130 | | | | 135 | | | 140 | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Thr | Lys | Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Cys | Ser | Arg |
| 145 | | | | | 150 | | | 155 | | | 160 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | Ser | Glu | Ser | Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys | Asp | Tyr |
| | 165 | | | | 170 | | | 175 | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Pro | Glu | Pro | Val | Thr | Val | Ser | Trp | Asn | Ser | Gly | Ala | Leu | Thr | Ser |
| | 180 | | | | 185 | | | 190 | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Val | His | Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser | Ser | Gly | Leu | Tyr | Ser |
| | 195 | | | | 200 | | | 205 | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Ser | Val | Val | Thr | Val | Pro | Ser | Ser | Asn | Phe | Gly | Thr | Gln | Thr |
| | 210 | | | | 215 | | | 220 | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Thr | Cys | Asn | Val | Asp | His | Lys | Pro | Ser | Asn | Thr | Lys | Val | Asp | Lys |
| | 225 | | | | 230 | | | 235 | | | 240 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Val | Glu | Arg | Lys | Cys | Cys | Val | Glu | Cys | Pro | Pro | Cys | Pro | Ala | Pro |
| | 245 | | | | 250 | | | 255 | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Val | Ala | Gly | Pro | Ser | Val | Phe | Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp |
| | 260 | | | | 265 | | | 270 | | | | | | | |

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Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 275 280 285
 Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
 290 295 300
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
 305 310 315 320
 Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
 325 330 335
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
 340 345 350
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
 355 360 365
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
 370 375 380
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 385 390 395 400
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 405 410 415
 Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 420 425 430
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 435 440 445
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 450 455 460
 Ser Leu Ser Pro Gly Lys
 465 470

<210> SEQ ID NO 228
 <211> LENGTH: 1410
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Polynucleotide
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <223> OTHER INFORMATION: Humanized Antibody Sequence

 <400> SEQUENCE: 228

| | | | | | | |
|-------------|-------------|-------------|-------------|------------|------------|-----|
| atggactgga | cctggaggat | cctttcttg | gtggcagcag | ccacaggagc | ccactccgag | 60 |
| gtgcagctgg | tgcagtctgg | ggctgaggtg | aagaagcctg | gggcctcagt | gaaggcttcc | 120 |
| tgcaaggctt | ctgacttcaa | cattaaagac | ttcttatctac | actgggtgcg | acaggcccct | 180 |
| ggacaagggc | ttgagtggt | tggaaggatt | gatcctgaga | atggtgatac | tttatatgac | 240 |
| ccgaagtcc | aggacaaggt | caccatgacc | acagacacgt | ccaccagcac | agcctacatg | 300 |
| gagctgagga | gcctgagatc | tgacgacacg | gccgtgtatt | actgtgcgag | agaggcgat | 360 |
| tatttccacg | atggtaacctc | ctactggta | ttcgatgtct | ggggccgtgg | caccctggtc | 420 |
| accgtctcta | gtgcctccac | caaggggcca | tcggtgttcc | ccctggcgcc | ctgtccagg | 480 |
| agcacctccg | agagcacagc | ggccctgggc | tgcctggta | aggactactt | ccccgaaccg | 540 |
| gtgacggtgt | cgtggaaactc | aggcgctcg | accagcggcg | tgcacacctt | cccagctgtc | 600 |
| ctacagtccct | caggactcta | ctccctcagc | agcgtggta | ccgtgcctc | cagcaacttc | 660 |
| ggcacccaga | octacacctg | caacgttagat | cacaagccca | gcaacaccaa | ggtggacaag | 720 |
| acagttgagc | gcaaatgttg | tgtcgagtgc | ccaccgtgcc | cagcaccacc | tgtggcagga | 780 |
| ccgtcagtct | tcctttccc | ccccaaaccc | aaggacaccc | tcatgatctc | ccggaccct | 840 |

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gagggtcacgt gcgtgggtggt ggacgtgagc cacgaagacc ccgaggtcca gttcaactgg      900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cacgggagga gcagtcaac      960
agcacgttcc gtgtggtcag cgtcttcacc gttgtgcacc aggactggct gaacggcaag     1020
gagtacaagt gcaaggcttc caacaaaggc ctcccagccc ccatcgagaa aaccatctcc     1080
aaaaccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag     1140
atgaccaaga accaggtcag cctgacctgc ctggtaaaag gtttctaccc cagcgacatc     1200
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac acctccatg     1260
ctggactccg acggctcctt cttectctac agcaagctca ccgtggacaa gagcaggtgg     1320
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg     1380
cagaagagcc tctccctgtc tccgggtaaa                                         1410

```

```

<210> SEQ ID NO 229
<211> LENGTH: 213
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 229

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```

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1           5          10          15

```

```

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Ile Ser Tyr Ile
20          25          30

```

```

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
35          40          45

```

```

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50          55          60

```

```

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65          70          75          80

```

```

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asp Pro Leu Thr
85          90          95

```

```

Phe Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100         105         110

```

```

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115         120         125

```

```

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130         135         140

```

```

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145         150         155         160

```

```

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165         170         175

```

```

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180         185         190

```

```

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195         200         205

```

```

Asn Arg Gly Glu Cys
210

```

```

<210> SEQ ID NO 230
<211> LENGTH: 639

```

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```

<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 230
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgttaggaga cagagtcacc      60
atcacttgca gggccagctc aagtataagt tacatacact ggtatcagca aaaaccaggg      120
aaagcccccta agctcctgat ctatgccaca tccaacctgg cttctggggt cccatcaagg      180
ttcagcggca gtggatctgg gacagaattc actctcacaa tcagcagcct gcagcctgaa      240
gattttgcaa cttattactg tcagcagtttgg agtagtgacc cactcacgtt cggcggagg      300
accaagggtgg agatcaaacg tacggtggt gcaccatctg tcttcatctt cccgcacatct      360
gatgagcagt tgaaatctgg aactgcctct gtttgtgccc tgctgaataa cttctatccc      420
agagaggcga aagtacagtg gaagggtggat aacgcgcctcc aatcggttaa ctcccaggag      480
agtgtcagc agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg      540
agcaaagcag actacgagaa acacaaagtc tacgcctgctg aagtcaaccca tcagggcctg      600
agctcgcccg tcacaaagag cttcaacagg ggagagtgt                                639

```

```

<210> SEQ ID NO 231
<211> LENGTH: 235
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 231
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp
1           5          10          15
Leu Pro Gly Ala Arg Cys Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe
20          25          30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
35          40          45
Ser Ser Ile Ser Tyr Ile His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
50          55          60
Pro Lys Leu Leu Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
65          70          75          80
Ser Arg Phe Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
85          90          95
Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp
100         105         110
Ser Ser Asp Pro Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
115         120         125
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130         135         140
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145         150         155         160
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165         170         175
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser

```

-continued

180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

| | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Val | Thr | Lys | Ser | Phe | Asn | Arg | Gly | Glu | Cys |
| 225 | | | | | 230 | | | | | 235 |

```
<210> SEQ ID NO 232
<211> LENGTH: 705
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody Sequence
```

<400> SEQUENCE: 232

| | | | | | | |
|-------------|--------------|-------------|-------------|------------|-------------|-----|
| atggacatga | gggtccccgc | tcagtcctcg | gggctcctgc | tgctctggct | cccagggtcc | 60 |
| agatgtgaca | tccagttgac | ccagtctcca | tccttcctgt | ctgcacatgt | aggagacaga | 120 |
| gtcaccatca | cttgcgaggc | cagctcaagt | ataagttaca | tacactggta | tcagcaaaaa | 180 |
| ccagggaaag | cccctaagct | cctgatctat | gccacatcca | acctggcttc | tggggtccca | 240 |
| tcaagggttca | gcggcagttgg | atctgggaca | gaattcactc | tcacaatcag | cagcctgcag | 300 |
| cctgaagatt | ttgcaactt | ttactgtcag | cagtggagta | gtgaccact | cacgttccgc | 360 |
| ggagggacca | aggtggagat | caaacgtacg | gtggctgcac | catctgtctt | catttcccg | 420 |
| ccatctgtat | agcagttgaa | atctggaaact | gcctctgttg | tgtgcctgct | gaataacttc | 480 |
| tatcccagag | aggccaaagt | acagtggaaag | gtggataacg | ccctccaatc | gggtaactcc | 540 |
| caggagatgt | tcacagagca | ggacagcaag | gacagcacct | acagcctcag | cagcacccctg | 600 |
| acgctgagca | aagcagacta | cgagaaacac | aaagtctacg | cctgcgaagt | caccatcat | 660 |
| qqqctqaqct | cqcccccgtcac | aaaqaqcttc | aaacaqqqqaq | aqtgt | | 705 |

```
<210> SEQ ID NO 233
<211> LENGTH: 447
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence
```

-400- SEQUENCE 223

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asp Ile Lys Asp Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Arg Val Asp Pro Asp Asn Gly Glu Thr Glu Phe Ala Pro Lys Phe
50 55 60

Pro Gly Lys Val Thr Met Thr Thr Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

US 9,089,553 B2

279**280**

-continued

Ala Arg Glu Asp Tyr Asp Gly Thr Tyr Thr Trp Phe Pro Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
 130 135 140
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190
 Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
 210 215 220
 Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
 385 390 395 400
 Asp Gly Ser Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
 405 410 415
 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

```

<210> SEQ ID NO 234
<211> LENGTH: 1341
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 234
  
```

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| | | | | | | |
|--------------|-------------|-------------|-------------|-------------|------------|------|
| gaggtgcagc | tggtcagtc | tggggcttag | gtgaagaagc | ctggggcctc | agtgaaggc | 60 |
| tcttgcagg | tttctggatt | cgcacattaag | gactactata | tacactgggt | gcgacaggcc | 120 |
| cctggacaag | ggcttgagt | gatcggaagg | gttgatctg | acaatggtga | gactgaattt | 180 |
| cccccaagt | tcccgccaa | ggtcaccatg | accacagaca | cgtccatcag | cacagcctac | 240 |
| atggagctga | gcaggctgag | atctgacgc | acggccgtgt | attactgtgc | gagagaagac | 300 |
| tcagatggta | cttacacctg | gtttccttat | tggggccaag | ggactctggt | caccgtctct | 360 |
| agtgcctcca | ccaaggggcc | atcggtcttc | ccctggcgc | cctgctccag | gagcacctcc | 420 |
| gagagcacag | cggccctggg | ctgcctggtc | aaggactact | tcccccgaacc | ggtgacggtg | 480 |
| tcgttggact | caggcgctct | gaccagcggc | gtgcacacct | tcccagctgt | cctacagtc | 540 |
| tcaggactct | actccctcag | cagcgtggtg | accgtgccct | ccagcaactt | cgccaccag | 600 |
| acctacacct | gcaacgtaga | tcacaagccc | agcaacacca | aggtggacaa | gacagttgag | 660 |
| cgcaaatgtt | gtgtcgagt | cccaccgtgc | ccagcaccac | ctgtggcagg | accgtcagtc | 720 |
| ttccctttcc | ccccaaaacc | caaggacacc | ctcatgtatct | cccgacccccc | tgaggtcacg | 780 |
| tgctgttgttgg | ttggacgtgag | ccacgaagac | cccgagggtcc | agttcaactg | gtacgtggac | 840 |
| ggcgtggagg | tgcataatgc | caagacaaag | ccacgggagg | agcagttcaa | cagcacgttc | 900 |
| cgtgttgtca | gcgtcctcac | cgtgtgcac | caggactggc | tgaacggcaa | ggagtacaag | 960 |
| tgcaaggctt | ccaacaaagg | cctcccaagcc | cccatcgaga | aaaccatctc | caaaacccaa | 1020 |
| gggcagccccc | gagaaccaca | ggtgtacacc | ctgccccat | ccggggagga | gatgaccaag | 1080 |
| aaccaggctca | gcctgacctg | cctggtcaaa | ggcttctacc | ccagcgcacat | cgccgtggag | 1140 |
| tgggagagca | atgggcagcc | ggagaacaac | tacaagacca | cacccat | gctggactcc | 1200 |
| gacggctctt | tcttcctcta | cagcaagctc | accgtggaca | agagcaggtg | gcagcagggg | 1260 |
| aacgtcttct | atgctccgt | gatgcatgag | gctctgcaca | accactacac | gcagaagagc | 1320 |
| ctctccctgt | ctccggtaaa | a | | | | 1341 |

<210> SEQ_ID NO 235

<211> LENGTH: 466

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 235

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Trp | Thr | Trp | Arg | Ile | Leu | Phe | Leu | Val | Ala | Ala | Ala | Thr | Gly |
| 1 | | | | | | 5 | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | His | Ser | Glu | Val | Gln | Leu | Val | Gln | Ser | Gly | Ala | Glu | Val | Lys | Lys |
| | | | | | | 20 | | | 25 | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Ala | Ser | Val | Lys | Val | Ser | Cys | Lys | Ala | Ser | Gly | Phe | Asp | Ile |
| | | | | | | 35 | | | 40 | | | | 45 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asp | Tyr | Tyr | Ile | His | Trp | Val | Arg | Gln | Ala | Pro | Gly | Gln | Gly | Leu |
| | | | | | | 50 | | | 55 | | | | 60 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Trp | Ile | Gly | Arg | Val | Asp | Pro | Asp | Asn | Gly | Glu | Thr | Glu | Phe | Ala |
| | | | | | | 65 | | | 70 | | | 75 | | 80 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Lys | Phe | Pro | Gly | Lys | Val | Thr | Met | Thr | Thr | Asp | Thr | Ser | Ile | Ser |
| | | | | | | 85 | | | 90 | | | 95 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Tyr | Met | Glu | Leu | Ser | Arg | Leu | Arg | Ser | Asp | Asp | Thr | Ala | Val |
| | | | | | | 100 | | | 105 | | | | 110 | | |

-continued

Tyr Tyr Cys Ala Arg Glu Asp Tyr Asp Gly Thr Tyr Thr Trp Phe Pro
115 120 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
145 150 155 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
195 200 205

Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn
210 215 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg
225 230 235 240

Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
275 280 285

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
290 295 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
305 310 315 320

Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys
325 330 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu
340 345 350

Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385 390 395 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met
405 410 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
420 425 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460

Gly Lys
465

```

<210> SEQ_ID NO 236
<211> LENGTH: 1398
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature

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-continued

<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 236

| | | | | | | |
|-------------|-------------|-------------|------------|------------|------------|------|
| atggactgga | cctggaggat | cctttcttg | gtggcagcag | ccacaggagc | ccactccgag | 60 |
| gtcagctgg | tgcagtctgg | ggctgaggtg | aagaagcctg | gggcctca | gaaggtctcc | 120 |
| tgcaaggctt | ctggattcga | cattaaggac | tactatac | actgggtcg | acaggccc | 180 |
| ggacaagggc | ttgagtggat | cggaaagggtt | gatcctgaca | atggtgagac | tgaatttgcc | 240 |
| ccgaagttcc | cggcaaggt | caccatgacc | acagacacgt | ccatcagcac | agcctacatg | 300 |
| gagctgagca | ggctgagatc | tgacgacacg | gccgtgtatt | actgtgcgag | agaagactac | 360 |
| gtatggta | accttgggtt | tccttattgg | ggccaaggga | ctctggtcac | cgtctctagt | 420 |
| gcctccacca | aggccccatc | ggtcttcccc | ctggcgcc | gtccaggag | caccccgag | 480 |
| agcacacgcg | ccctgggctg | cctggtaag | gactactcc | ccgaaccggt | gacggtgctg | 540 |
| tggaaactcag | gcgcctctgac | cagcggcgt | cacaccc | cagctgtc | acagtcctca | 600 |
| ggactctact | ccctcagcag | cgtggtgacc | gtgcctcca | gcaactcgg | cacccagacc | 660 |
| tacacctgca | acgttagatca | caagccc | aacccaagg | tggacaagac | agttgagcgc | 720 |
| aaatgttgc | tcgagtgc | accgtgc | gcaccac | tggcaggacc | gtcagtctc | 780 |
| ctcttcccc | aaaaacccaa | ggacacc | atgatctcc | ggaccc | gtcacgtc | 840 |
| gtgggttgtt | acgtgagcca | cgaagac | gaggtcc | tcaactgg | cgtggac | 900 |
| gtggagggtgc | ataatgcca | gacaaagcca | cggaggag | agttcaac | cacgtcc | 960 |
| gtgggtcagcg | tcctcacc | tgtgcacc | gactgg | acggcaag | gtacaag | 1020 |
| aaggctcca | acaaaggc | cccagcccc | atcgagaaa | ccatctcc | aaccaaagg | 1080 |
| cagcccc | aaccacag | gtacacc | ccccatccc | gggaggag | gaccaag | 1140 |
| caggtcagcc | tgacctgc | ggtcaaagg | ttctaccc | gcgacat | cgtggag | 1200 |
| gagagcaatg | ggcagccg | gaacaact | aagacc | ctccatg | ggactcc | 1260 |
| ggctcttct | tcctctac | caagtcacc | gtggaca | gcaggtgg | gcaggg | 1320 |
| gtcttctcat | gtccgtgat | gcatgagg | ctgcaca | actacac | gaagac | 1380 |
| tcctgtctc | cggtaaa | | | | | 1398 |

<210> SEQ ID NO 237

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 237

| | | | | | | |
|-----|-----|-----|-----|---|-----|-----|
| Gly | Thr | Ser | Asn | L | Ala | Ser |
| 1 | | | | 5 | | |

<210> SEQ ID NO 238

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 238

| | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Gln | Trp | Thr | Thr | Thr | Tyr | Thr |
| 1 | | | | 5 | | | |

<210> SEQ ID NO 239

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

-continued

<400> SEQUENCE: 239

```
Arg Ala Ser Gln Asp Ile Ser Ser Tyr Leu Asn
1           5           10
```

<210> SEQ ID NO 240

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 240

```
Ser Thr Ser Arg Leu Asn Ser
1           5
```

<210> SEQ ID NO 241

<211> LENGTH: 8

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 241

```
Gln Gln Asp Ile Lys His Pro Thr
1           5
```

<210> SEQ ID NO 242

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 242

```
Lys Ala Ser Gln Asp Val Phe Thr Ala Val Ala
1           5           10
```

<210> SEQ ID NO 243

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 243

```
Trp Ala Ser Thr Arg His Thr
1           5
```

<210> SEQ ID NO 244

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 244

```
Gln Gln Tyr Ser Ser Tyr Pro Leu Thr
1           5
```

<210> SEQ ID NO 245

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 245

```
Asp Tyr Asn Met His
1           5
```

<210> SEQ ID NO 246

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 246

-continued

Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe Lys
 1 5 10 15

Gly

<210> SEQ ID NO 247
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 247

Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val
 1 5 10

<210> SEQ ID NO 248
 <211> LENGTH: 5
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 248

Asp Tyr Asn Met His
 1 5

<210> SEQ ID NO 249
 <211> LENGTH: 17
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 249

Glu Ile Asn Pro Asn Ser Gly Gly Ser Gly Tyr Asn Gln Lys Phe Lys
 1 5 10 15

Gly

<210> SEQ ID NO 250
 <211> LENGTH: 14
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 250

Leu Val Tyr Asp Gly Ser Tyr Glu Asp Trp Tyr Phe Asp Val
 1 5 10

<210> SEQ ID NO 251
 <211> LENGTH: 5
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 251

Asp Tyr Asn Met His
 1 5

<210> SEQ ID NO 252
 <211> LENGTH: 17
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 252

Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Gln Phe Lys
 1 5 10 15

Gly

<210> SEQ ID NO 253
 <211> LENGTH: 14

-continued

<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 253

Leu Gly Tyr Val Gly Asn Tyr Glu Asp Trp Tyr Phe Asp Val
1 5 10

<210> SEQ ID NO 254
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 254

Asp Tyr Asn Met His
1 5

<210> SEQ ID NO 255
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 255

Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> SEQ ID NO 256
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 256

Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val
1 5 10

<210> SEQ ID NO 257
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 257

Asp Tyr Asn Met His
1 5

<210> SEQ ID NO 258
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 258

Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> SEQ ID NO 259
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 259

Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val
1 5 10

-continued

<210> SEQ ID NO 260
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 260

Asp Tyr Asn Met His
1 5

<210> SEQ ID NO 261
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 261

Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe Lys
1 5 10 15

GLY

<210> SEQ ID NO 262
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 262

Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val
1 5 10

<210> SEQ ID NO 263
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 263

Asp Tyr Asn Met His
1 5

<210> SEQ ID NO 264
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 264

Glu Ile Asn Pro Asn Ser Gly Gly Ser Gly Tyr Asn Gln Lys Phe Lys
1 5 10 15

GLY

<210> SEQ ID NO 265
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 265

Leu Gly Tyr Tyr Gly Asn Tyr Glu Asp Trp Tyr Phe Asp Val
1 5 10

<210> SEQ ID NO 266
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 266

Asp Tyr Tyr Ile His
1 5

-continued

<210> SEQ_ID NO 267
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 267

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ile | Asp | Pro | Asp | Asn | Gly | Glu | Ser | Thr | Tyr | Val | Pro | Lys | Phe | Gln |
| | | | | | | | | | | | | | | | |
| 1 | | | | | | | | | | | | | | | 15 |

Gly

<210> SEQ_ID NO 268
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 268

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|----|
| Glu | Gly | Leu | Asp | Tyr | Gly | Asp | Tyr | Tyr | Ala | Val | Asp | Tyr | | |
| | | | | | | | | | | | | | | |
| 1 | | | | | | | | | | | | | | 10 |

<210> SEQ_ID NO 269
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 269

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|---|
| Asp | Tyr | Ile | Met | His | | | | | | | | | | |
| | | | | | | | | | | | | | | |
| 1 | | | | | | | | | | | | | | 5 |

<210> SEQ_ID NO 270
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 270

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ile | Asn | Pro | Tyr | Asn | Asp | Asp | Thr | Glu | Tyr | Asn | Glu | Lys | Phe | Lys |
| | | | | | | | | | | | | | | | |
| 1 | | | | | | | | | | | | | | | 15 |

Gly

<210> SEQ_ID NO 271
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 271

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|----|
| Ser | Ile | Tyr | Tyr | Tyr | Asp | Ala | Pro | Phe | Ala | Tyr | | | | | |
| | | | | | | | | | | | | | | | |
| 1 | | | | | | | | | | | | | | | 10 |

<210> SEQ_ID NO 272
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 272

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|---|
| Asp | Tyr | Tyr | Met | His | | | | | | | | | | |
| | | | | | | | | | | | | | | |
| 1 | | | | | | | | | | | | | | 5 |

<210> SEQ_ID NO 273
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 273

-continued

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ile | Asp | Pro | Glu | Asn | Gly | Asp | Ile | Ile | Tyr | Asp | Pro | Lys | Phe | Gln |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |

Gly

<210> SEQ ID NO 274

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 274

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|
| Asp | Ala | Gly | Asp | Pro | Ala | Trp | Phe | Thr | Tyr | | | | | | |
| 1 | | | | 5 | | | 10 | | | | | | | | |

<210> SEQ ID NO 275

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 275

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|
| Arg | Ala | Ser | Ser | Ser | Val | Tyr | Tyr | Met | His | | | | | | |
| 1 | | | | 5 | | | | 10 | | | | | | | |

<210> SEQ ID NO 276

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 276

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|
| Ala | Thr | Ser | Asn | Leu | Ala | Ser | | | | | | | | | |
| 1 | | | | 5 | | | | | | | | | | | |

<210> SEQ ID NO 277

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 277

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|
| Gln | Gln | Trp | Ser | Ser | Asp | Pro | Leu | Thr | | | | | | | |
| 1 | | | | 5 | | | | | | | | | | | |

<210> SEQ ID NO 278

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 278

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Ser | Val | Ser | Ser | Thr | Ile | Ser | Ser | Asn | His | Leu | His | | | | |
| 1 | | | | 5 | | | | | 10 | | | | | | |

<210> SEQ ID NO 279

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 279

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|
| Gly | Thr | Ser | Asn | Leu | Ala | Ser | | | | | | | | | |
| 1 | | | | 5 | | | | | | | | | | | |

<210> SEQ ID NO 280

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 280

-continued

Gln Gln Trp Ser Ser Tyr Pro Leu Thr
1 5

<210> SEQ ID NO 281
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 281

Arg Ala Ser Ser Ser Ile Ser Tyr Ile His
1 5 10

<210> SEQ ID NO 282
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 282

Ala Thr Ser Asn Leu Ala Ser
1 5

<210> SEQ ID NO 283
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 283

Gln Gln Trp Ser Ser Asp Pro Leu Thr
1 5

<210> SEQ ID NO 284
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 284

Arg Ala Ser Ser Ser Val Thr Ser Ser Tyr Leu Asn
1 5 10

<210> SEQ ID NO 285
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 285

Ser Thr Ser Asn Leu Ala Ser
1 5

<210> SEQ ID NO 286
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 286

Gln Gln Tyr Asp Phe Phe Pro Ser Thr
1 5

<210> SEQ ID NO 287
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 287

Asp Tyr Phe Ile His
1 5

-continued

<210> SEQ_ID NO 288
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 288

Arg Leu Asp Pro Glu Asp Gly Glu Ser Asp Tyr Ala Pro Lys Phe Gln
1 5 10 15

Asp

<210> SEQ_ID NO 289
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 289

Glu Asp Tyr Asp Gly Thr Tyr Thr Phe Phe Pro Tyr
1 5 10

<210> SEQ_ID NO 290
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 290

Asp Phe Tyr Leu His
1 5

<210> SEQ_ID NO 291
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 291

Arg Ile Asp Pro Glu Asn Gly Asp Thr Leu Tyr Asp Pro Lys Phe Gln
1 5 10 15

Asp

<210> SEQ_ID NO 292
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 292

Glu Ala Asp Tyr Phe His Asp Gly Thr Ser Tyr Trp Tyr Phe Asp Val
1 5 10 15

<210> SEQ_ID NO 293
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 293

Asp Tyr Tyr Ile His
1 5

<210> SEQ_ID NO 294
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 294

-continued

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Val | Asp | Pro | Asp | Asn | Gly | Glu | Thr | Glu | Phe | Ala | Pro | Lys | Phe | Pro |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |

Gly

<210> SEQ ID NO 295

<211> LENGTH: 12

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 295

| | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asp | Tyr | Asp | Gly | Thr | Tyr | Thr | Trp | Phe | Pro | Tyr |
| 1 | | | | 5 | | | | 10 | | | |

<210> SEQ ID NO 296

<211> LENGTH: 5

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 296

| | | | | |
|-----|-----|-----|-----|-----|
| Asp | Tyr | Tyr | Met | Asn |
| 1 | | | 5 | |

<210> SEQ ID NO 297

<211> LENGTH: 17

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 297

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Asn | Pro | Tyr | Asn | Asp | Asp | Thr | Thr | Tyr | Asn | His | Lys | Phe | Lys |
| 1 | | | | 5 | | | | 10 | | | | 15 | | | |

Gly

<210> SEQ ID NO 298

<211> LENGTH: 11

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 298

| | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Thr | Ala | Val | Ile | Thr | Thr | Asn | Ala | Met | Asp |
| 1 | | | 5 | | | | | 10 | | |

<210> SEQ ID NO 299

<211> LENGTH: 130

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 299

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Phe | Gln | Val | Gln | Ile | Phe | Ser | Phe | Met | Leu | Ile | Ser | Val | Thr |
| 1 | | | | 5 | | | 10 | | | 15 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Leu | Ser | Ser | Gly | Glu | Ile | Val | Leu | Thr | Gln | Ser | Pro | Ala | Leu |
| | 20 | | | | 25 | | | | 30 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ser | Pro | Gly | Glu | Lys | Val | Thr | Ile | Thr | Cys | Ser | Val | Ser |
| | 35 | | | 40 | | | 45 | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Ile | Ser | Ser | Ser | Asn | Leu | His | Trp | Ser | Gln | Gln | Lys | Ser | Gly |
| | 50 | | | 55 | | | 60 | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Pro | Lys | Leu | Trp | Ile | Tyr | Gly | Thr | Ser | Asn | Leu | Ala | Ser | Gly |
| 65 | | | | 70 | | | 75 | | | | 80 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Val | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Ser | Tyr | Ser | Leu |
| | 85 | | | 90 | | | 95 | | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ile | Ser | Ser | Met | Glu | Ala | Glu | Asp | Ala | Ala | Thr | Tyr | Tyr | Cys | Gln |
| | 100 | | | 105 | | | 110 | | | | | | | | |

-continued

Gln Trp Thr Thr Tyr Thr Phe Gly Ser Gly Thr Lys Leu Glu Leu
 115 120 125

Lys Arg
130

<210> SEQ ID NO 300

<211> LENGTH: 390

<212> TYPE: DNA

<213> ORGANISM: *Mus musculus*

<400> SEQUENCE: 300

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| atggatttgc | agggtgcagat | tttcagcttc | atgctaata | gtgtcacagt | catattgtcc | 60 |
| agtggagaaa | tttgtgtcac | ccagtcctcca | gcactcatgg | ctgcacatccc | aggggagaag | 120 |
| gttccacatca | cctgcgtgtgt | cagtcgtcgt | ataagttcca | gcaacttaca | ctggtccccag | 180 |
| cagaagtcag | gaacctcccc | caaactctgg | atttatggca | catccaaacct | tgcttctgg | 240 |
| gtccctgttc | gttctcgtgg | cagtggatct | gggaccttct | atttctctcac | aatcagcagc | 300 |
| atggagggtcg | aagatgtgc | cacttattac | tgtcaaacagt | ggactactac | gtatacgttc | 360 |
| ggatcggggg | ccaaagtcgga | gctgaaacgt | | | | 390 |

<210> SEQ ID NO 301

<211> LENGTH: 141

<212> TYPE: PRT

<213> ORGANISM: *Mus musculus*

<400> SEQUENCE: 301

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Trp | Asn | Trp | Ile | Ile | Phe | Phe | Leu | Met | Ala | Val | Val | Thr | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Ser | Glu | Val | Gln | Leu | Arg | Gln | Ser | Gly | Ala | Asp | Leu | Val | Lys |
| 20 | | | | | | | | 25 | | | | | | 30 | |

Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
35 40 45

Lys Asp Tyr Tyr Ile His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu
 50 55 60

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Trp | Ile | Gly | Arg | Ile | Asp | Pro | Asp | Asn | Gly | Glu | Ser | Thr | Tyr | Val |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |

Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn
85 90 95

Thr Ala Tyr Leu Gln Leu Arg Ser Leu Thr Ser Glu Asp Thr Ala Ile
100 105 110

Tyr Tyr Cys Gly Arg Glu Gly Leu Asp Tyr Gly Asp Tyr Tyr Ala Val
115 120 125

| | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Tyr | Trp | Gly | Gln | Gly | Thr | Ser | Val | Thr | Val | Ser | Ser |
| 130 | | | | | | 135 | | | | | 140 | |

<210> SEQ ID NO 302

<211> LENGTH: 423

<212> TYPE: DNA

<213> ORGANISM: *Mus musculus*

<400> SEQUENCE: 302

| | | | | | | |
|-------------|------------|--------------|-------------|------------|------------|-----|
| atggggatgga | actggatcat | cttcttcctg | atggcagtgg | ttacaggggt | caattcagag | 60 |
| gtgcagttgc | ggcagtctgg | ggcagacacctt | gtgaaggccag | gggcctcagt | caagtgtcc | 120 |
| tgcacagctt | ctgggttcaa | cattaaagac | tactataac | actgggtgaa | gcagaggcct | 180 |
| gaacaggggc | tggagtggat | tggaggatt | gatcctgata | atggtaaag | tacatatgtc | 240 |

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| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ccgaagttcc | aggccaaggc | cactataaca | gcagacacat | catccaacac | agcctaccta | 300 |
| caactcgaaa | gcctgacatc | tgaggacact | gccatctatt | attgtggag | agagggctc | 360 |
| gactatggtg | actactatgc | tgtggactac | tggggtaaag | gaacctcggt | cacagtctcg | 420 |
| agc | | | | | | 423 |

<210> SEQ ID NO 303
<211> LENGTH: 130
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence
<400> SEQUENCE: 303

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Met | Arg | Val | Pro | Ala | Gln | Leu | Leu | Gly | Leu | Leu | Leu | Leu | Trp |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Leu | Pro | Gly | Ala | Arg | Cys | Asp | Ile | Gln | Leu | Thr | Gln | Ser | Pro | Ser | Phe |
| | | | | | | 20 | | 25 | | | | | | 30 | |
| Leu | Ser | Ala | Ser | Val | Gly | Asp | Arg | Val | Thr | Ile | Thr | Cys | Ser | Val | Ser |
| | | | | 35 | | | 40 | | | | | | | 45 | |
| Ser | Ser | Ile | Ser | Ser | Ser | Asn | Leu | His | Trp | Tyr | Gln | Gln | Lys | Pro | Gly |
| | | | | | | 50 | | 55 | | | | | | 60 | |
| Lys | Ala | Pro | Lys | Leu | Leu | Ile | Tyr | Gly | Thr | Ser | Asn | Leu | Ala | Ser | Gly |
| | | | | | | 65 | | 70 | | | | | | 80 | |
| Val | Pro | Ser | Arg | Phe | Ser | Gly | Ser | Gly | Thr | Glu | Phe | Thr | Leu | | |
| | | | | | | 85 | | 90 | | | | | | 95 | |
| Thr | Ile | Ser | Ser | Leu | Gln | Pro | Glu | Asp | Phe | Ala | Thr | Tyr | Tyr | Cys | Gln |
| | | | | | | 100 | | 105 | | | | | | 110 | |
| Gln | Trp | Thr | Thr | Thr | Tyr | Thr | Phe | Gly | Gln | Gly | Thr | Lys | Leu | Glu | Ile |
| | | | | | | 115 | | 120 | | | | | | 125 | |
| Lys | Arg | | | | | | | | | | | | | | |
| | 130 | | | | | | | | | | | | | | |

<210> SEQ ID NO 304
<211> LENGTH: 390
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody Sequence
<400> SEQUENCE: 304

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| atggatatgc | gcgtgcggc | gcagctgctg | ggcctgctgc | tgctgtggct | gccgggcgcg | 60 |
| cgctgcgata | ttcagctgac | ccagagcccg | agctttctga | gcgcgagcgt | ggcgatcgc | 120 |
| gtgaccatta | cctgcagcgt | gagcagcgc | attagcagca | gcaacctgca | ttggtatcag | 180 |
| cagaaacccg | gcaaagcgcc | gaaactgctg | atttatggca | ccagcaacct | ggcgagccgc | 240 |
| gtgccgagcc | gctttagcgg | cagcggcgc | ggcacccgaat | ttaccctgac | cattagcagc | 300 |
| ctgcagccgg | aagattttgc | gacctattat | tgccagcagt | ggaccaccac | ctataccctt | 360 |
| ggccaggcga | ccaaactgga | aattaaacgt | | | | 390 |

<210> SEQ ID NO 305
<211> LENGTH: 141

-continued

```

<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 305

Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Pro Thr Gly
1           5          10          15

Ala His Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20          25          30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile
35          40          45

Lys Asp Tyr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50          55          60

Glu Trp Met Gly Arg Ile Asp Pro Asp Asn Gly Glu Ser Thr Tyr Val
65          70          75          80

Pro Lys Phe Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85          90          95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100         105         110

Tyr Tyr Cys Ala Arg Glu Gly Leu Asp Tyr Gly Asp Tyr Tyr Ala Val
115         120         125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130         135         140

<210> SEQ ID NO 306
<211> LENGTH: 423
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 306

atggatttga cctggagcat tctgtttctg gtggcgccgc cgaccggcgc gcatagcgaa      60
gtgcagctgg tgcagagcgg cgccggaaatg aaaaaacccgg ggcgcgacgt gaaaatgtggc      120
tgcaaaacgca gcggcttaa cattaaatgt tattatattc attgggtgcg ccaggcgccg      180
ggccaggccc tggaaatggat gggccgcatt gatccggata acggcgaaag cacctatgt      240
ccgaaatttc agggccgcgt gaccatgacc accgatacca gcaccagcac cgcttatatg      300
gaactgcgcga gcctgcgcag cgatgatacc gccgtgtatt attgcgcgcg cgaaggctg      360
gattatggcg attattatgc ggtggattat tggggccagg gcacccttgtt gaccgtctcg      420
agc                                         423

<210> SEQ ID NO 307
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 307

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Ser | Ser | Ala | Gln | Phe | Leu | Gly | Leu | Leu | Leu | Cys | Phe | Gln | |
| 1 | | | | 5 | | | 10 | | | | | 15 | | | |
| Gly | Thr | Arg | Cys | Asp | Ile | Gln | Met | Thr | Gln | Thr | Thr | Ser | Ser | Leu | Ser |
| | | | | 20 | | | 25 | | | | | 30 | | | |
| Ala | Ser | Leu | Gly | Asp | Arg | Val | Asn | Ile | Ser | Cys | Arg | Ala | Ser | Gln | Asp |
| | | | | 35 | | | 40 | | | | 45 | | | | |
| Ile | Ser | Ser | Tyr | Leu | Asn | Trp | Tyr | Gln | Gln | Lys | Pro | Asp | Gly | Thr | Val |
| | | | | 50 | | | 55 | | | | 60 | | | | |
| Lys | Leu | Leu | Ile | Tyr | Ser | Thr | Ser | Arg | Leu | Asn | Ser | Gly | Val | Pro | Ser |
| | | | | 65 | | | 70 | | | | 75 | | | 80 | |
| Arg | Phe | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Asp | Tyr | Ser | Leu | Thr | Ile | Ser |
| | | | | 85 | | | 90 | | | | 95 | | | | |
| Asn | Leu | Ala | Gln | Glu | Asp | Ile | Ala | Thr | Tyr | Phe | Cys | Gln | Gln | Asp | Ile |
| | | | | 100 | | | 105 | | | | 110 | | | | |
| Lys | His | Pro | Thr | Phe | Gly | Gly | Thr | Lys | Leu | Glu | Leu | Lys | Arg | | |
| | | | | 115 | | | 120 | | | | 125 | | | | |

<210> SEQ_ID NO 308

<211> LENGTH: 381

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 308

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| atgatgtcct | ctgctcagtt | ccttggcttc | ctgttgctct | gttttcaagg | taccagatgt | 60 |
| gatatccaga | tgacacagac | tacatcctcc | ctgtctgcct | ctctggaga | cagagtcaac | 120 |
| atcagctgca | ggccaagtca | ggacatttgc | agttatttaa | actggatca | gcagaaacca | 180 |
| gatggaactg | ttaaactcct | gatctactcc | acatcaagat | taaactcagg | agtcccatca | 240 |
| aggttcagtg | gcagtgggtc | tgggacat | tattctctca | ctattagcaa | cctggcacaa | 300 |
| gaagatattg | ccacttactt | ttgccaacag | gatattaagc | atccgacgtt | cggtggaggc | 360 |
| accaagttgg | agctgaaacg | t | | | | 381 |

<210> SEQ_ID NO 309

<211> LENGTH: 139

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 309

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Trp | Ile | Trp | Ile | Phe | Leu | Phe | Leu | Leu | Ser | Gly | Thr | Ala | Gly |
| 1 | | | | 5 | | | 10 | | | | 15 | | | | |
| Val | His | Ser | Glu | Val | Gln | Leu | Gln | Ser | Gly | Pro | Glu | Leu | Val | Lys | |
| | | | | 20 | | | 25 | | | | 30 | | | | |
| Pro | Gly | Ala | Ser | Val | Lys | Met | Ser | Cys | Lys | Ala | Ser | Gly | Phe | Thr | Phe |
| | | | | 35 | | | 40 | | | | 45 | | | | |
| Thr | Asp | Tyr | Ile | Met | His | Trp | Val | Lys | Gln | Lys | Pro | Gly | Gln | Gly | Leu |
| | | | | 50 | | | 55 | | | | 60 | | | | |
| Glu | Trp | Ile | Gly | Tyr | Ile | Asn | Pro | Tyr | Asn | Asp | Asp | Thr | Glu | Tyr | Asn |
| | | | | 65 | | | 70 | | | | 75 | | | 80 | |
| Glu | Lys | Phe | Lys | Gly | Lys | Ala | Thr | Leu | Thr | Ser | Asp | Lys | Ser | Ser | Ser |
| | | | | 85 | | | 90 | | | | 95 | | | | |
| Thr | Ala | Tyr | Met | Asp | Leu | Ser | Ser | Leu | Thr | Ser | Glu | Gly | Ser | Ala | Val |
| | | | | 100 | | | 105 | | | | 110 | | | | |
| Tyr | Tyr | Cys | Ala | Arg | Ser | Ile | Tyr | Tyr | Tyr | Asp | Ala | Pro | Phe | Ala | Tyr |
| | | | | 115 | | | 120 | | | | 125 | | | | |
| Trp | Gly | Gln | Gly | Thr | Leu | Val | Thr | Val | Ser | Ser | | | | | |

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130

135

```

<210> SEQ ID NO 310
<211> LENGTH: 417
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 310
atggaatgga tctggatatt tctttcctc ctgtcaggaa ctgcaggtgt ccactctgag      60
gtccagctgc agcagtctgg acctgagctg gtaaagcctg gggcttcaagt gaagatgtcc    120
tgcaaggcct ctgggttcac attcaactgac tacattatgc actgggtgaa gcagaaggcct    180
gggcagggcc ttgagtggat tggatataatt aatccttaca atgatgatac tgaataacaat    240
gagaagttca aaggcaaggc cacactgact tcagacaaaat cctccagcac agcctacatg    300
gatctcagca gtctgacctc tgagggctct gcggcttatt actgtgcaag atcgatttat    360
tactacgatg ccccgttgc ttactggggc caagggactc tggcacagt ctcgagc      417

```

```

<210> SEQ ID NO 311
<211> LENGTH: 127
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence

```

```

<400> SEQUENCE: 311
Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Cys Phe Gln
1           5          10          15

Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20          25          30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
35          40          45

Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
50          55          60

Lys Leu Leu Ile Tyr Ser Thr Ser Arg Leu Asn Ser Gly Val Pro Ser
65          70          75          80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85          90          95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Cys Gln Gln Asp Ile
100         105         110

Lys His Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
115         120         125

```

```

<210> SEQ ID NO 312
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody Sequence

```

```

<400> SEQUENCE: 312
atgatgtctt ctgctcagtt cttgggtctc ctgttgcctt gtttcaagg taccagatgt      60
gatatccaga tgaccaggc tccatccctc ctgtctgcat ctgttaggtga ccgtgtcacc    120
atcacttgcc gcgcaagtca ggatattac agctattaa attggatatac gcagaaacca    180

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gggaaaagccc ctaagtcct gatctattct acttcccggt tgaatagtg ggccccatca      240
cgcttcagtgc acgtggctc tgggacagat ttcaactctca ccatcagcag tctgcaacct      300
gaagattttg caacttacta ctgtcaacag gatattaaac accctacggtt cggtcaaggc      360
accaagggtgg agatcaaacg t                                         381

```

```

<210> SEQ_ID NO 313
<211> LENGTH: 139
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 313

```

```

Met Glu Trp Ile Trp Ile Phe Leu Phe Leu Ser Gly Thr Ala Gly
1           5           10          15

Val His Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20          25          30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
35          40          45

Thr Asp Tyr Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50          55          60

Glu Trp Met Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn
65          70          75          80

Glu Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
85          90          95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100         105         110

Tyr Tyr Cys Ala Arg Ser Ile Tyr Tyr Asp Ala Pro Phe Ala Tyr
115         120         125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130         135

```

```

<210> SEQ_ID NO 314
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 314
Asp Ile Gln Met Thr Gln Thr Ser Ser Leu Ser Ala Ser Leu Gly
1           5           10          15

Asp Arg Val Asn Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr
20          25          30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35          40          45

Tyr Ser Thr Ser Arg Leu Asn Ser Gly Val Pro Ser Arg Phe Ser Gly
50          55          60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Ala Gln
65          70          75          80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asp Ile Lys His Pro Thr
85          90          95

Phe Gly Gly Thr Lys Leu Glu Leu Lys Arg
100         105

```

-continued

<210> SEQ ID NO 315
<211> LENGTH: 128
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 315

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ser | Gln | Thr | Gln | Val | Phe | Val | Tyr | Met | Leu | Leu | Trp | Leu | Ser |
| 1 | | | | | | 5 | | | | 10 | | | | 15 | |

Gly Val Glu Gly Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser
20 25 30

Thr Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
35 40 45

Val Phe Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
50 55 60

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp
65 70 75 80

Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser
100 105 110

Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
115 120 125

<210> SEQ ID NO 316
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 316

| | | | | | | | |
|------------|------------|-------------|------------|------------|------------|---|-----|
| atgaagtac | agaccagg | cgttgcata | atgttgctgt | ggttgtctgg | tgttgaagg | a | 60 |
| gacattgt | tgaccagg | tcacaaattc | atgtccacgt | cagtaggaga | cagggtcacc | | 120 |
| atcacctg | aggccagg | ca ggtgtctt | actgctgtag | cctggtatca | acagaaacca | | 180 |
| ggacaatct | ctaaactact | gatTTactgg | gcattccacc | ggcacactgg | agtccctgat | | 240 |
| cgcttcacag | gcagtggatc | tgggacagat | ttcactctca | ccattagcaa | tgtgcagtct | | 300 |
| gaagacttgg | cagattattt | ctgtcaacaa | tatagcagct | atcctctcac | gttcgggtct | | 360 |
| gggaccaagt | tggagctgaa | a | | | | | 381 |

<210> SEQ ID NO 317
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 317

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Trp | Asn | Trp | Ile | Ile | Phe | Phe | Leu | Met | Ala | Val | Val | Thr | Gly |
| 1 | | | | | 5 | | | | 10 | | | | 15 | | |

Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

Pro Gly Ala Leu Val Lys Leu Ser Cys Lys Ala Ser Gly Phe Asn Ile
35 40 45

Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu
50 55 60

Glu Trp Ile Gly Arg Ile Asp Pro Glu Asn Gly Asp Ile Ile Tyr Asp
65 70 75 80

Pro Lys Phe Gln Gly Lys Ala Ser Ile Thr Thr Asp Thr Ser Ser Asn
85 90 95

-continued

Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Tyr Asp Ala Gly Asp Pro Ala Trp Phe Thr Tyr Trp
115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130 135

<210> SEQ ID NO 318

<211> LENGTH: 411

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 318

| | |
|--|-----|
| atgggatgga actggatcat cttttcctg atggcagtgg ttacaggggt caattcagag | 60 |
| gttcagtcg acgactctgg ggctgagctt gtgaggccag gggccttagt caagttgtcc | 120 |
| tgc当地 agctt ctggcttcaa tattaaagac tactatatgc actgggtgaa gcagaggcct | 180 |
| gaacagggcc tggagtggat tggaggatt gatcctgaga atggtgatata tatatatgac | 240 |
| ccgaagttcc agggcaaggc cagtataaca acagacacat cctccaacac agcctacctg | 300 |
| cagctcagca gcctgacgta tgaggacact gccgtctatt actgtgttta cgatgttgtt | 360 |
| gacccccgcct ggtttactta ctggggccaa gggactctgg tcaccgtctc g | 411 |

<210> SEQ ID NO 319

<211> LENGTH: 130

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 319

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
35 40 45

Gln Asp Val Phe Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val
65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
100 105 110

Tyr Ser Ser Tyr Pro Leu Thr Phe Gly Gly Thr Lys Val Glu Ile
115 120 125

Lys Arg
130

<210> SEQ ID NO 320

<211> LENGTH: 390

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 320

| | |
|--|-----|
| atggatatgc gcgtgcggc gcagctgctg ggccctgctgc tgctgtggct ggcggcgcg | 60 |
| cgctgcgata tccagatgac ccagagcccg agcagcctga ggcgcgacgtt gggcgatcgc | 120 |
| gtgaccattta cctgcaaagc gagccaggat gtgtttacgg cggtggcggt gtatcagcag | 180 |

-continued

```

aaaccgggca aagcgccgaa actgctgatt tattgggcga gcacccgcca taccggcgtg      240
ccgagtcgtt tttagcggcag cggcagcggc accgattta ccctgaccat tagcagcctg      300
cagccggaag attttgcgac ctattattgc cagcagtata gcagctatcc gctgaccttt      360
ggcggggca ccaaagtgg aattaaacgt                                390

```

```

<210> SEQ_ID NO 321
<211> LENGTH: 138
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 321

```

```

Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Pro Thr Gly
1           5           10          15

Ala His Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20          25          30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile
35          40          45

Lys Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50          55          60

Glu Trp Ile Gly Arg Ile Asp Pro Glu Asn Gly Asp Ile Ile Tyr Asp
65          70          75          80

Pro Lys Phe Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser
85          90          95

Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val
100         105         110

Tyr Tyr Cys Ala Tyr Asp Ala Gly Asp Pro Ala Trp Phe Thr Tyr Trp
115         120         125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
130         135

```

```

<210> SEQ_ID NO 322
<211> LENGTH: 414
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 322

```

```

atggatttggaa octggaggcat tctgtttctg gtggcggcgc cgaccggcgc gcatagcgaa      60
gtgcagctgg tgcagagcgg cgcggaaatg aaaaaacccgg ggcgcgacgt gaaagtggc          120
tgcaaaacgca gcggctttaa cattaaagat tattatatgc attgggtgcg ccaggcggc          180
ggccaggccc tgaaatggat cggccgcatt gatccggaaa acggcgatat tatttatgat          240
ccgaaatttc agggccgcgt gaccatgacc accgatacca gcaccagcac cgcgtatatg          300
gaaactgcgca gcctgcgcag cgatgatacc gcggtgtatt attgcgcgta tgatgcggc          360
gatccggcgt ggtttaccta ttggggccag ggcaccctgg tgaccgtctc gagc          414

```

```

<210> SEQ_ID NO 323
<211> LENGTH: 106

```

-continued

<212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 323

```

Thr Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
1           5          10          15

Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
20          25          30

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
35          40          45

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
50          55          60

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
65          70          75          80

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
85          90          95

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
100          105
  
```

<210> SEQ_ID NO 324
 <211> LENGTH: 320
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 324

```

Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
1           5          10          15

Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
20          25          30

Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
35          40          45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
50          55          60

Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
65          70          75          80

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
85          90          95

Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro
100         105         110

Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
115         120         125

Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser
130         135         140

Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu
145         150         155         160

Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr
165         170         175

Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn
180         185         190

Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro
195         200         205

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln
210         215         220

Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val
225         230         235         240
  
```

US 9,089,553 B2

325**326**

-continued

Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val
 245 250 255

Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln
 260 265 270

Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn
 275 280 285

Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val
 290 295 300

Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
 305 310 315 320

<210> SEQ ID NO 325

<211> LENGTH: 106

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 325

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1 5 10 15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 20 25 30

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 35 40 45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 50 55 60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 65 70 75 80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 85 90 95

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 100 105

<210> SEQ ID NO 326

<211> LENGTH: 327

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 326

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
 65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
 100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 130 135 140

-continued

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 145 150 155 160
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205
 Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 210 215 220
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 275 280 285
 Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 305 310 315 320
 Leu Ser Leu Ser Leu Gly Lys
 325

<210> SEQ_ID NO 327
 <211> LENGTH: 120
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <400> SEQUENCE: 327
 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asp Tyr
 20 25 30
 Ile Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Asp Leu Ser Ser Leu Thr Ser Glu Gly Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Ser Ile Tyr Tyr Asp Ala Pro Phe Ala Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> SEQ_ID NO 328
 <211> LENGTH: 120
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <400> SEQUENCE: 328
 Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

US 9,089,553 B2

329**330**

-continued

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asp Tyr
 20 25 30

Ile Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Asp Leu Ser Ser Leu Thr Ser Glu Gly Ser Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Ser Ile Tyr Tyr Asp Ala Pro Phe Ala Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 329

<211> LENGTH: 120

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 329

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asp Tyr
 20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Ser Ile Tyr Tyr Asp Ala Pro Phe Ala Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 330

<211> LENGTH: 226

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 330

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asp Tyr
 20 25 30

Ile Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Asp Leu Ser Ser Leu Thr Ser Glu Gly Ser Ala Val Tyr Tyr Cys
 85 90 95

-continued

Ala Arg Ser Ile Tyr Tyr Asp Ala Pro Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Thr Val Ala Ala Pro Ser Val Phe
115 120 125

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
130 135 140

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
145 150 155 160

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
165 170 175

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
180 185 190

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
195 200 205

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
210 215 220

Glu Cys
225

<210> SEQ ID NO 331
<211> LENGTH: 447
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 331

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asp Tyr
20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ile Tyr Tyr Asp Ala Pro Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
225 230 235 240

-continued

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> SEQ ID NO 332
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 332

Asp Ile Gln Met Thr Gln Ile Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Ser Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Phe Lys Leu Leu Ile
35 40 45

Phe Tyr Thr Ser Arg Leu Leu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Tyr Asn Leu Glu Gln
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asp Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> SEQ ID NO 333
<211> LENGTH: 324
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 333

Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
1 5 10 15

-continued

Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
 20 25 30
 Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
 50 55 60
 Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
 65 70 75 80
 Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
 85 90 95
 Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro
 100 105 110
 Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
 115 120 125
 Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser
 130 135 140
 Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu
 145 150 155 160
 Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr
 165 170 175
 Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn
 180 185 190
 Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro
 195 200 205
 Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln
 210 215 220
 Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val
 225 230 235 240
 Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val
 245 250 255
 Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln
 260 265 270
 Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn
 275 280 285
 Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val
 290 295 300
 Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
 305 310 315 320
 Ser Pro Gly Lys

<210> SEQ ID NO 334
 <211> LENGTH: 213
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus

<400> SEQUENCE: 334

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15
 Asp Arg Val Asn Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45
 Tyr Ser Thr Ser Arg Leu Asn Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

-continued

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Ala Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Asp Ile Lys His Pro Thr
85 90 95

Phe Gly Gly Thr Lys Leu Glu Leu Lys Arg Thr Asp Ala Ala Pro
100 105 110

Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly
115 120 125

Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn
130 135 140

Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn
145 150 155 160

Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser
165 170 175

Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr
180 185 190

Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe
195 200 205

Asn Arg Asn Glu Cys
210

<210> SEQ ID NO 335
<211> LENGTH: 444
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 335

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asp Tyr
20 25 30

Ile Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Thr Ser Glu Gly Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ile Tyr Tyr Tyr Asp Ala Pro Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
115 120 125

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
130 135 140

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
145 150 155 160

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
180 185 190

Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala
195 200 205

Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys

US 9,089,553 B2

339**340**

-continued

210 215 220

Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe
 225 230 235 240

Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val
 245 250 255

Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe
 260 265 270

Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro
 275 280 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro
 290 295 300

Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val
 305 310 315 320

Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
 325 330 335

Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys
 340 345 350

Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp
 355 360 365

Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro
 370 375 380

Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser
 385 390 395 400

Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala
 405 410 415

Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His
 420 425 430

His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 435 440

<210> SEQ ID NO 336

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 336

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Phe Thr Ala
 20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Ser Tyr Pro Leu
 85 90 95

Thr Phe Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> SEQ ID NO 337

<211> LENGTH: 324

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

-continued

<400> SEQUENCE: 337

| | | | | | | |
|-------------|-------------|-------------|------------|-------------|------------|-----|
| gatatccaga | tgacccagag | cccgaggcgc | ctgagcgcga | gcgtggcga | tcgcgtgacc | 60 |
| attacctgca | aagcgagcca | ggatgtgtt | accgcggtgg | cgtggtatca | gcagaaaccg | 120 |
| ggcaaagcgc | cgaaaactgct | gatttattgg | gcgagcaccc | gccataccgg | cgtgcggagt | 180 |
| cgcttttagcg | gcagcggcag | cggcacccat | tttaccctga | ccattagcag | cctgcagccg | 240 |
| gaagattttgc | cgaccttatta | ttgcacagcag | tatagcagct | atccgcgtgac | ctttggccgc | 300 |
| ggcacccaaag | tggaaattaa | acgt | | | | 324 |

<210> SEQ ID NO 338

<211> LENGTH: 119

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 338

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Val | Gln | Ser | Gly | Ala | Glu | Val | Lys | Lys | Pro | Gly | Ala |
| 1 | | | | 5 | | | | 10 | | | 15 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Lys | Val | Ser | Cys | Lys | Ala | Ser | Gly | Phe | Asn | Ile | Lys | Asp | Tyr |
| | | | | | 20 | | | 25 | | | | 30 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Met | His | Trp | Val | Arg | Gln | Ala | Pro | Gly | Gln | Gly | Leu | Glu | Trp | Ile |
| | 35 | | | | 40 | | | | 45 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Arg | Ile | Asp | Pro | Glu | Asn | Gly | Asp | Ile | Ile | Tyr | Asp | Pro | Lys | Phe |
| | 50 | | | | 55 | | | 60 | | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Gly | Arg | Val | Thr | Met | Thr | Thr | Asp | Thr | Ser | Thr | Ser | Thr | Ala | Tyr |
| 65 | | | | | 70 | | | 75 | | | 80 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Arg | Ser | Leu | Arg | Ser | Asp | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |
| | 85 | | | | 90 | | | | 95 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Tyr | Asp | Ala | Gly | Asp | Pro | Ala | Trp | Phe | Thr | Tyr | Trp | Gly | Gln | Gly |
| | | 100 | | | | 105 | | | | 110 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|
| Thr | Leu | Val | Thr | Val | Ser | Ser | | | | | | | | | |
| | | | | | 115 | | | | | | | | | | |

<210> SEQ ID NO 339

<211> LENGTH: 357

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 339

| | | | | | | |
|-------------|--------------|------------|------------|------------|------------|-----|
| gaagtgcagc | tggtcagag | cggcgccgaa | gtgaaaaaac | cgggcgcgag | cgtgaaagt | 60 |
| agctgcggaa | cggcgccgtt | taacattaaa | gattattata | tgcattgggt | gcgcaggcg | 120 |
| ccggggccagg | gccttggaaatg | gatcgccgc | attgatccgg | aaaacggcga | tattattat | 180 |
| gatccgaaat | ttcaggcccc | cgtgaccatg | accaccata | ccagcaccag | caccgcgtat | 240 |
| atggaaactgc | gcagectgcg | cagcgatgt | accgcggtgt | attattgcgc | gtatgtgcg | 300 |
| ggcgatccgg | cgtggtttac | ctattggggc | cagggcaccc | tggtgaccgt | ctcgagc | 357 |

<210> SEQ ID NO 340

<211> LENGTH: 1395

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 340

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| atggactgga | cctggaggat | cctttcttg | gtggcagcag | ccacaggagc | ccactccgag | 60 |
| gtgcagctgg | tgcagtctgg | ggctgagggt | aagaagctg | ggtcctcggt | gaaggctcc | 120 |
| tgcaaggctt | ctggtttac | cttcaccgac | tatattatgc | actgggtgcg | tcaggcccct | 180 |

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ggtaaaggcc ttgagtggat gggctatac aaccctata atgatgacac cgaatacaca 240
gagaagttca agggccgtgt cacgattacc gcggacaaat ccacgagcac agcctacatg 300
gagctgagca ggcgtggctc tgaggacacg gccgtgtatt actgtggcg ttcgatttat 360
tactacgtat ccccggttgc ttactgggc caagggactc tggtaaccgt ctctagtgcc 420
tccaccaagg gccccatcggt cttcccccgt gcgcctgtt ccaggagcac ctccgagagc 480
acagcggccc tgggtgtcgt ggtcaaggac tacttccccc aaccgggtgac ggtgtcg 540
aactcaggcg ctctgaccag cgccgtgcac accttcccag ctgtccata gtcctcgaga 600
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca acttcggcac ccagacctac 660
acctgtcaacg tagatcacaa gcccagcaac accaagggtgg acaagacagt tgaggc 720
tgttgtgtcg agtgcccacc gtgcccagca ccacctgtgg caggaccgtc agtcttc 780
ttcccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacgtcg 840
gtgggtggacg tgagccacga agaccccgag gtccagttca actggtagt ggacggcg 900
gagggtgcata atgccaagac aaagccacgg gaggagcagt tcaacagcac gttccgtgt 960
gtcagcgtcc tcaccgttgt gcaccaggac tggctgaacg gcaaggagta caagtgc 1020
gtctccaaca aaggccatccc agccccatc gagaaaaacca tctccaaaac caaaggcg 1080
ccccgagaac cacaggtgta caccctggcc ccatcccgaa aggagatgac caagaaccag 1140
gtcagcgtga cctgcgttgtt caaaggcttc taccctcagcg acatgcgtt ggagtggag 1200
agcaatgggc agccggagaa caactacaag accacaccc tcgttgcgtt ccgtcg 1260
tccttctcc tctacagcaa gtcaccgtg gacaagagca ggtggcagca gggaaacgtc 1320
ttctcatgtt ccgtgtatgca tgaggctctg cacaaccactt acacgcagaa gagctctcc 1380
ctgtctccgg qtaaa 1395

<210> SEQ ID NO 341

<211> LENGTH: 213

<212> TYPE: PRT

<213> ORGANISM: *Mus musculus*

<400> SEQUENCE: 341

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala | Ser | Val | Gly |
| 1 | | | | | 5 | | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Val | Thr | Ile | Thr | Cys | Arg | Ala | Ser | Gln | Asp | Ile | Ser | Ser | Tyr |
| | | | 20 | | | | 25 | | | | | 30 | | | |

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Thr Ser Arg Leu Asn Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Ile Lys His Pro Thr
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu

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| | | | |
|---|-----|-----|-----|
| 145 | 150 | 155 | 160 |
| Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser | | | |
| 165 | 170 | 175 | |
| Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala | | | |
| 180 | 185 | 190 | |
| Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe | | | |
| 195 | 200 | 205 | |
| Asn Arg Gly Glu Cys | | | |
| 210 | | | |

<210> SEQ ID NO 342

<211> LENGTH: 639

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 342

| | |
|--|-----|
| gacatccaga tgaccaggc tccatcctcc ctgtctgc ctgttaggtga ccgtgtcacc | 60 |
| atcacttgcc gcgcaagtca ggatatttgc agctatttaa atttggatca gcagaaacca | 120 |
| gggaaaagccc ctaagtcctt gatctatttc acttcccggt tgaatagtgg ggtccccatca | 180 |
| cgttccatgt gcagtggtc tgggacagat ttcaacttc caatcagcag tctgcaacct | 240 |
| gaagattttgc caacttacta ctgtcaacag gatattaaac accctacgtt cggtcaaggc | 300 |
| accaagggtgg agatcaaacg tacgggtggct gcaccatctg ttttcatctt cccggcatct | 360 |
| gtatggcgtt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc | 420 |
| agagaggcca aagtacagtgc gaagggtggat aacgcccctcc aatcgggtaa ctcccaggag | 480 |
| agtgtcacag agcaggacagc caaggacagc acctacagcc tcagcagcac cctgacgctg | 540 |
| accaaaggcag actacagagaa acacaaagtc tacgcctgcg aagtccacca tcagggcctg | 600 |
| agtcgccccg tcacaaagag cttcaacagg ggagagtgt | 639 |

<210> SEQ ID NO 343

<211> LENGTH: 235

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 343

| | | | |
|---|-----|-----|----|
| Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp | | | |
| 1 | 5 | 10 | 15 |
| Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser | | | |
| 20 | 25 | 30 | |
| Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser | | | |
| 35 | 40 | 45 | |
| Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys | | | |
| 50 | 55 | 60 | |
| Ala Pro Lys Leu Leu Ile Tyr Ser Thr Ser Arg Leu Asn Ser Gly Val | | | |
| 65 | 70 | 75 | 80 |
| Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr | | | |
| 85 | 90 | 95 | |
| Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln | | | |
| 100 | 105 | 110 | |
| Asp Ile Lys His Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys | | | |
| 115 | 120 | 125 | |
| Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu | | | |
| 130 | 135 | 140 | |

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Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> SEQ_ID NO 344

<211> LENGTH: 705

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 344

atggacatga ggggtgcccgc tcagtcctcg gggctcctgc tgctgtggct gagagggtgcc 60
 agatgtgaca tccagatgac ccagtctcca tcctccctgt ctgcattctgt aggtgaccgt 120
 gtcaccatca cttggccgcgc aagtccaggat attagcagct atttaaatgg gtatcagcag 180
 aaaccaggaa aagccccctaa gctcctgatc tattctactt cccgtttgaa tagtggggtc 240
 ccatcacgct tcagtgccag tggctctggg acagattca ctctcaccat cagcagctg 300
 caacacctgaag attttgcAAC ttactactgt caacaggata ttaaacaccc tacgttcgg 360
 caaggcacca aggtggagat caaacgtacg gtggctgcac catctgtctt catttcccg 420
 ccatctgtat agcagttgaa atcttggaaact gcctctgtt tttgcctgtt gaataacttc 480
 tatcccagag aggccaaagt acagtggaaat gtggataacg ccctccaatc gggtaactcc 540
 caggagatgt tcacagagca ggacagcaag gacagcacctt acagcctcag cagcaccc 600
 acgctgagca aaggcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 660
 ggccctgagct cgcccgatcac aaagagcttc aacaggggag agtgt 705

<210> SEQ_ID NO 345

<211> LENGTH: 446

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 345

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asp Tyr
 20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Ser Ile Tyr Tyr Asp Ala Pro Phe Ala Tyr Trp Gly Gln
 100 105 110

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Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
210 215 220

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
290 295 300

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> SEQ ID NO 346

<211> LENGTH: 1338

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 346

gaggtgcagc tgggtcagtc tggggcttagt gtgaagaagc ctgggtccctc ggtgaaggtc 60

tccctgcagg cttctggtt taccttcacc gactatatta tgcactgggt gcgtcaggcc 120

cctggtcaag ggcttgagtg gatgggctat atcaaccctt ataatgtga caccgaatac 180

aacgagaagt tcaaggcccg tgtcacgatt accgcggaca aatccacgag cacagcctac 240

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| | |
|--|------|
| atggagctga gcagectgcg ctctgaggac acggccgtgt | 300 |
| tattactacg atgccccgtt tgcttactgg ggccaaggga ctctggtcac | 360 |
| cgtctctagt gcctccacca agggeccatc ggtttcccc ctggcgccct | 420 |
| gtccaggag cacctccag agcacagcg ccctgggtcg cctggtcaag | 480 |
| gactactcc cacacccatc gactacttc cagaaccggg gacgggttcg | 540 |
| tggaacttag cgctctgac cagcggcggt cacacccatc cagctgtctt | 600 |
| acagtcctca ggactctact ccctcagcag cgtggtgacc gtgccttcca | 660 |
| gcaacttcgg cacccagacc tacacctgca acgtagatca caagcccagc | 720 |
| aacaccaagg tggacaagac agttgagcgc aaatgttgcg tcgagtgccc | 780 |
| accgtgccc gcaccacctg tggcaggacc gtcagtcttc ctcttcccc | 840 |
| caaaaaccaa ggacacccctc atgatctccc ggacccctga ggtcacgtgc | 900 |
| gtgggggtgg acgtgagcca cgaagacccc gaggtccagt tcaactggta | 960 |
| cgtggacggc gtggaggtgc ataatgccaa gacaaagcca cgggaggagc | 1020 |
| agttcaacag cacgtccgt gtggcagcg tcctcaccgt tggcaccag | 1080 |
| gactggctga acggcaagga gtacaagtgc aaggctccca acaaaggcct | 1140 |
| cccagcccc atcgagaaaa ccatctccaa aaccaaaggg cagccccgag | 1200 |
| aaccacaggt gtacacccctg ccccccattcc gggaggagat gaccaagaac | 1260 |
| cagggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc | 1320 |
| cgtggagtgcc gggggaaac gtcttctcat gtcctgtat gcatgaggct | 1380 |
| ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaa | 1338 |

<210> SEQ_ID NO 347

<211> LENGTH: 465

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 347

| | | | | |
|---|---|---|----|----|
| Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala | 1 | 5 | 10 | 15 |
|---|---|---|----|----|

| | | | |
|---|----|----|----|
| Ala His Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys | 20 | 25 | 30 |
|---|----|----|----|

| | | | |
|---|----|----|----|
| Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe | 35 | 40 | 45 |
|---|----|----|----|

| | | | |
|---|----|----|----|
| Thr Asp Tyr Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu | 50 | 55 | 60 |
|---|----|----|----|

| | | | | |
|---|----|----|----|----|
| Glu Trp Met Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn | 65 | 70 | 75 | 80 |
|---|----|----|----|----|

| | | | |
|---|----|----|----|
| Glu Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser | 85 | 90 | 95 |
|---|----|----|----|

| | | | |
|---|-----|-----|-----|
| Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val | 100 | 105 | 110 |
|---|-----|-----|-----|

| | | | |
|---|-----|-----|-----|
| Tyr Tyr Cys Ala Arg Ser Ile Tyr Tyr Asp Ala Pro Phe Ala Tyr | 115 | 120 | 125 |
|---|-----|-----|-----|

| | | | |
|---|-----|-----|-----|
| Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly | 130 | 135 | 140 |
|---|-----|-----|-----|

| | | | | |
|---|-----|-----|-----|-----|
| Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser | 145 | 150 | 155 | 160 |
|---|-----|-----|-----|-----|

| | | | |
|---|-----|-----|-----|
| Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val | 165 | 170 | 175 |
|---|-----|-----|-----|

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Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 180 185 190

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 195 200 205

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
 210 215 220

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
 225 230 235 240

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
 245 250 255

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 260 265 270

Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp
 275 280 285

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 290 295 300

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
 305 310 315 320

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
 325 330 335

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
 340 345 350

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 355 360 365

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 370 375 380

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 385 390 395 400

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
 405 410 415

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 420 425 430

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 435 440 445

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 450 455 460

Lys
 465

<210> SEQ ID NO 348

<211> LENGTH: 1395

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 348

atggactgga cctggaggat cctttcttg gtggcagcag ccacaggagc ccactccag 60

gtgcagctgg tgcagtctgg ggctgagggt aagaagcctg ggtcctcggt gaaggctc 120

tgcaggctt ctggtttac cttcacccgac tatattatgc actgggtgcg tcaggccc 180

ggtaaggcc ttgagtgat gggctatac aacccttata atgatgacac cgaataaca 240

gagaagttca agggccgtgt cacgattacc gcggacaaat ccacgagcac agcctacat 300

gagctgagca gcctgcgcgc tgaggacacg gccgtgtatt actgtgcgcg ttgcattat 360

tactacgatg cccccgttgc ttactggggc caagggactc tggtcaccgt ctctagtgcc 420

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355**356**

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| | |
|--|------|
| tccaccaagg gccccatcggt ctteccccctg ggcgcctgct ccaggagcac ctccgagac | 480 |
| acagcggccc tgggctgcct ggtcaaggac tacttcccc aaccgggtgac ggtgtcggtgg | 540 |
| aactcaggcg ctctgaccag cggegtgcac accttcccag ctgtctaca gtcctcagga | 600 |
| ctctactccc tcagcagcgt ggtgaccgtg ccctccagca acttcggcac ccagacctac | 660 |
| acctgcaacg tagatcacaa gcccagcaac accaagggtgg acaagacagt tgagcgcaaa | 720 |
| tgttgtgtcg agtgeccacc gtgeccagca ccacctgtgg caggaccgtc agtcttcctc | 780 |
| ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacgtcggtg | 840 |
| gtgggtggacg tgagccacga agaccccgag gtccagttca actggtagtgg ggacggcggtg | 900 |
| gaggtgcata atgccaagac aaagccacgg gaggagcagt tcaacagcac gttccgtgtg | 960 |
| gtcagcgtcc tcaccgttgc gcaccaggac tggctgaacg gcaaggagta caagtgcag | 1020 |
| gtctccaaca aaggcctccc agccccatc gagaaaaacca tctccaaaac caaagggcag | 1080 |
| ccccgagaac cacagggtgt aaccctgccc ccatccccggg aggagatgac caagaaccag | 1140 |
| gtcagcgtga cctgcgttgcg taaaggcttc taccggcgtg acatcgccgt ggagtggag | 1200 |
| agcaatgggc agccggagaa caactacaag accacacctc ccatgtgttca ctccgacggc | 1260 |
| tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca gggaaacgtc | 1320 |
| ttctctatgtc ccgtgtatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc | 1380 |
| ctgtctccgg gtaaa | 1395 |

<210> SEQ ID NO 349

<211> LENGTH: 417

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 349

| | |
|---|-----|
| atggaatgga tctggatatt tcttttcctc ctgtcaggaa ctgcagggtgt ccactcttag | 60 |
| gtgcagctgg tgcagtctgg ggctgaggtg aagaagcctg ggtcctcggt gaaggctctcc | 120 |
| tgcaaggctt ctggttttac cttcaccgac tatattatgc actgggtgcg tcaggcccct | 180 |
| ggtcaaggcgc ttgagtggat gggctatatac aacccttatac atgatgacac cgaataacaac | 240 |
| gagaagttca agggccgtgt cacgattacc gcggacaaat ccacgagcac agcctacatg | 300 |
| gagctgagca gcctgcgttc tgaggacacg gccgtgtatt actgtgcgcg ttgcatttat | 360 |
| tactacgtg ccccggttgc ttactggggc caagggactc tggtcacagt ctcgagc | 417 |

<210> SEQ ID NO 350

<211> LENGTH: 218

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 350

| | |
|---|--|
| Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly | |
| 1 5 10 15 | |
| Gln Arg Ala Thr Ile Ala Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp | |
| 20 25 30 | |
| Gly Thr Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro | |
| 35 40 45 | |
| Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Glu Ile Pro Ala | |
| 50 55 60 | |
| Arg Phe Ser Gly Thr Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His | |
| 65 70 75 80 | |

US 9,089,553 B2

357**358**

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| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Val | Glu | Glu | Glu | Asp | Ile | Thr | Thr | Tyr | Tyr | Cys | Gln | Gln | Ser | Asn |
| | | | | | | 85 | | | 90 | | | | | 95 | |
| Glu | Asp | Pro | Phe | Thr | Phe | Gly | Gly | Gly | Thr | Lys | Leu | Glu | Ile | Lys | Arg |
| | | | | | | 100 | | | 105 | | | | | 110 | |
| Ala | Asp | Ala | Ala | Pro | Thr | Val | Ser | Ile | Phe | Pro | Pro | Ser | Ser | Glu | Gln |
| | | | | | | 115 | | | 120 | | | | | 125 | |
| Leu | Thr | Ser | Gly | Gly | Ala | Ser | Val | Val | Cys | Phe | Leu | Asn | Asn | Phe | Tyr |
| | | | | | | 130 | | | 135 | | | | | 140 | |
| Pro | Lys | Asp | Ile | Asn | Val | Lys | Trp | Lys | Ile | Asp | Gly | Ser | Glu | Arg | Gln |
| | 145 | | | | | 150 | | | | 155 | | | | 160 | |
| Asn | Gly | Val | Leu | Asn | Ser | Trp | Thr | Asp | Gln | Asp | Ser | Lys | Asp | Ser | Thr |
| | | | | | | 165 | | | 170 | | | | | 175 | |
| Tyr | Ser | Met | Ser | Ser | Thr | Leu | Thr | Leu | Thr | Lys | Asp | Glu | Tyr | Glu | Arg |
| | | | | | | 180 | | | 185 | | | | | 190 | |
| His | Asn | Ser | Tyr | Thr | Cys | Glu | Ala | Thr | His | Lys | Thr | Ser | Thr | Ser | Pro |
| | | | | | | 195 | | | 200 | | | | | 205 | |
| Ile | Val | Lys | Ser | Phe | Asn | Arg | Asn | Glu | Cys | | | | | | |
| | | 210 | | | 215 | | | | | | | | | | |

<210> SEQ ID NO 351

<211> LENGTH: 15

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 351

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Ser | Gln | Ser | Val | Asp | Tyr | Asp | Gly | Thr | Ser | Tyr | Met | Asn |
| 1 | | | | | | 5 | | | 10 | | | | 15 | |

<210> SEQ ID NO 352

<211> LENGTH: 7

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 352

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|
| Ala | Ala | Ser | Asn | Leu | Glu | Ser | | | | | | | | |
| 1 | | | | | 5 | | | | | | | | | |

<210> SEQ ID NO 353

<211> LENGTH: 9

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 353

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|
| Gln | Gln | Ser | Asn | Glu | Asp | Pro | Phe | Thr | | | | | | |
| 1 | | | | | | 5 | | | | | | | | |

<210> SEQ ID NO 354

<211> LENGTH: 657

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 354

| | | | | | | | |
|-------------|-------------|------------|-------------|-------------|------------|--|-----|
| gacattgtgt | tgacccagtc | tccagcttct | ttggctgtgt | ctctaggggca | gagggccacc | | 60 |
| | | | | | | | |
| atcgcctgca | aggccagcca | aagtgttcat | tatgtatggta | ctagttatat | gaattggtag | | 120 |
| | | | | | | | |
| caacagaaac | caggacagcc | acccaaactc | ctcatctatg | ctgcatacaa | tctagaatct | | 180 |
| | | | | | | | |
| gagatccccag | ccatgttttag | tggcactggg | tctgggacacg | acttcacccct | caacatccat | | 240 |
| | | | | | | | |
| cctgtggagg | aggaggatat | cacaacctat | tactgtcagc | aaagtaatga | ggatccgttc | | 300 |
| | | | | | | | |
| acgttcggag | gggggaccaa | gttggaaata | aaacgggctg | atgctgcacc | aactgtatcc | | 360 |
| | | | | | | | |

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```

atcttcccac catccagtga gcagttaca tctggaggcg cctcagtcgt gtgcttcgg 420
aacaacctct accccaaaga catcaatgtc aagtggaaata ttgatggcag tgaacgacaa 480
aatggcggtcc tgaacagttg gactgatcg gacagcaaag acagcaccta cagcatgagc 540
agcacccctca cggtgaccgg ggacgagttt gaacgcatac acagctatac ctgtgaggcc 600
actcacaaga catcaacttc acccattgtc aagagcttca acaggaatga gtgttag 657

```

<210> SEQ ID NO 355

<211> LENGTH: 238

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 355

```

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1      5          10          15

```

```

Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
20     25          30

```

```

Val Ser Leu Gly Gln Arg Ala Thr Ile Ala Cys Lys Ala Ser Gln Ser
35     40          45

```

```

Val Asp Tyr Asp Gly Thr Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
50     55          60

```

```

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
65     70          75          80

```

```

Glu Ile Pro Ala Arg Phe Ser Gly Thr Gly Ser Gly Thr Asp Phe Thr
85     90          95

```

```

Leu Asn Ile His Pro Val Glu Glu Asp Ile Thr Thr Tyr Tyr Cys
100    105         110

```

```

Gln Gln Ser Asn Glu Asp Pro Phe Thr Phe Gly Gly Thr Lys Leu
115    120         125

```

```

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
130    135         140

```

```

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
145    150         155         160

```

```

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
165    170         175

```

```

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
180    185         190

```

```

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
195    200         205

```

```

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
210    215         220

```

```

Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225    230         235

```

<210> SEQ ID NO 356

<211> LENGTH: 717

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 356

```

atggagacag acacaatcct gctatgggtg ctgctgtct gggttccagg ctccactgg 60

```

```

gacattgtgt tgacccagtc tccagttct ttggctgtgt ctctagggca gagggccacc 120

```

```

atcgcctgca aggccagcca aagtgttgat tatgtatggta ctatgttatat gaattggtag 180

```

```

caacagaaac caggacagcc acccaaactc ctcatctatg ctgcattccaa tcttagaatct 240

```

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gagatccag ccaggttag tggcaactggg tctggacag acttcaccct caacatccat 300
 cctgtggagg aggaggatat cacaacctat tactgtcagc aaagtaatga ggatccgttc 360
 acgttcggag gggggaccaa gttggaaata aaacgggctg atgctgcacc aactgtatcc 420
 atcttccccatccatcatcactga gcagttaca tctggaggtg ctcagtcgt gtgcttcttg 480
 aacaacttct accccaaaga catcaatgtc aagtggaaaga ttgatggcag tgaacgacaa 540
 aatggcgatcc tgaacagttg gactgtatcg gacagcaag acagcaccta cagcatgagc 600
 agcaccctca cggtgaccaa ggacgagttt gaacgacata acagctatac ctgtgaggcc 660
 actcacaaga catcaacttc acccattgtc aagagcttca acaggaatga gtgttag 717

<210> SEQ ID NO 357

<211> LENGTH: 442

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 357

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Val | Gln | Leu | Gln | Gln | Pro | Gly | Thr | Glu | Leu | Val | Arg | Pro | Gly | Thr |
| 1 | | | | | | | | | 10 | | | | | | 15 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Lys | Leu | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Ile | Phe | Thr | Thr | Tyr |
| 20 | | | | | | | | 25 | | | | | | | 30 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Met | Asn | Trp | Val | Lys | Gln | Arg | Pro | Gly | Gln | Gly | Leu | Glu | Trp | Ile |
| 35 | | | | | | | | 40 | | | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Met | Ile | His | Pro | Ser | Ala | Ser | Glu | Ile | Arg | Leu | Asp | Gln | Lys | Phe |
| 50 | | | | | | | | 55 | | | 60 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asp | Lys | Ala | Thr | Leu | Thr | Leu | Asp | Lys | Ser | Ser | Ser | Thr | Ala | Tyr |
| 65 | | | | | | | | 70 | | 75 | | | | | 80 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Leu | Ser | Gly | Pro | Thr | Ser | Val | Asp | Ser | Ala | Val | Tyr | Tyr | Cys |
| 85 | | | | | | | | 90 | | | 95 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Arg | Ser | Gly | Glu | Trp | Gly | Ser | Met | Asp | Tyr | Trp | Gly | Gln | Gly | Thr |
| 100 | | | | | | | | 105 | | | | 110 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Thr | Val | Ser | Ser | Ala | Lys | Thr | Thr | Pro | Pro | Ser | Val | Tyr | Pro |
| 115 | | | | | | | | 120 | | | 125 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | Pro | Gly | Ser | Ala | Ala | Gln | Thr | Asn | Ser | Met | Val | Thr | Leu | Gly |
| 130 | | | | | | | | 135 | | | 140 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Leu | Val | Lys | Gly | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val | Thr | Trp | Asn |
| 145 | | | | | | | | 150 | | 155 | | | | | 160 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Leu | Ser | Ser | Gly | Val | His | Thr | Phe | Pro | Ala | Val | Leu | Gln |
| 165 | | | | | | | | 170 | | | | | | | 175 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Asp | Leu | Tyr | Thr | Leu | Ser | Ser | Val | Thr | Val | Pro | Ser | Ser | Thr |
| 180 | | | | | | | | 185 | | | 190 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Pro | Ser | Glu | Thr | Val | Thr | Cys | Asn | Val | Ala | His | Pro | Ala | Ser | Ser |
| 195 | | | | | | | | 200 | | | 205 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Lys | Val | Asp | Lys | Lys | Ile | Val | Pro | Arg | Asp | Cys | Gly | Cys | Lys | Pro |
| 210 | | | | | | | | 215 | | | 220 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ile | Cys | Thr | Val | Pro | Glu | Val | Ser | Ser | Val | Phe | Ile | Phe | Pro | Pro |
| 225 | | | | | | | | 230 | | 235 | | | | | 240 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Pro | Lys | Asp | Val | Leu | Thr | Ile | Thr | Leu | Thr | Pro | Lys | Val | Thr | Cys |
| 245 | | | | | | | | 250 | | | | 255 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Val | Asp | Ile | Ser | Lys | Asp | Asp | Pro | Glu | Val | Gln | Phe | Ser | Trp |
| 260 | | | | | | | | 265 | | | 270 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Val | Asp | Asp | Val | Glu | Val | His | Thr | Ala | Gln | Thr | Gln | Pro | Arg | Glu |
| 275 | | | | | | | | 280 | | | 285 | | | | |

-continued

Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met
290 295 300

His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser
305 310 315 320

Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly
325 330 335

Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln
340 345 350

Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe
355 360 365

Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu
370 375 380

Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe
385 390 395 400

Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn
405 410 415

Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr
420 425 430

Glu Lys Ser Leu Ser His Ser Pro Gly Lys
435 440

<210> SEQ ID NO 358
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 358

Thr Tyr Trp Met Asn
1 5

<210> SEQ ID NO 359
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 359

Met Ile His Pro Ser Ala Ser Glu Ile Arg Leu Asp Gln Lys Phe Lys
1 5 10 15

Asp

<210> SEQ ID NO 360
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 360

Ser Gly Glu Trp Gly Ser Met Asp Tyr
1 5

<210> SEQ ID NO 361
<211> LENGTH: 1329
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 361

caggtccaac tacagcagcc tgggactgag ctgggtggcc ctggaaacctc agtgaagg 60
tcctgttaagg cttctggcta catcttcacc acctactgga tgaactgggt gaaacagagg 120
cctggacaag gccttgagtg gattggcatg attcatcctt ccgcagaatgt aatttagttg 180

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| | |
|---|------|
| gatcagaaat tcaaggacaa ggccacattg actcttgaca aatcctccag cacagcctat | 240 |
| atgcaccta gggcccgac atctgtggat tctgcccgtt attactgtgc aagatcagg | 300 |
| gaatgggggt ctatggacta ctggggtcaa ggaacctcag tcaccgtctc ctcagccaaa | 360 |
| acgacaccccc catctgtcta tccactggcc cctggatctg ctgcccaaac taactccatg | 420 |
| gtgaccctgg gatgectggt caagggctat ttccctgagc cagtgcacgt gacctggAAC | 480 |
| tctggatccc tgtccagcgg tgtgcacacc ttcccaagctg tcctgcagtc tgacccatc | 540 |
| actctgagca gtcagtgac tgtccctcc agcacctggc ccagcgagac cgtcacctgc | 600 |
| aacgttgcggcc acccgcccg cagcaccaag gtggacaaga aaatttgcc cagggatgt | 660 |
| ggttgttaagc cttgcatatg tacagtccca gaagtatcat ctgtcttcat ctcccccca | 720 |
| aagcccaagg atgtgtcac cattactctg actcctaagg tcacgtgtgt tggttagac | 780 |
| atcagcaagg atgatcccgaa ggtccagttc agctggttt tagatgtatgt ggagggtgcac | 840 |
| acagctcaga cgcaaccccg ggaggagcag ttcaacagca cttccgcctc agtcagtgaa | 900 |
| cttcccatca tgcaccagga ctggctcaat ggcaaggagt tcaaattgcag ggtcaacagt | 960 |
| gcagcttcc ctgccccat cgagaaaaacc atctccaaaa ccaaaggcag accgaaggct | 1020 |
| ccacagggtgt acaccattcc acctcccaag gagcagatgg ccaaggataa agtcagtgaa | 1080 |
| acctgcgtga taacagactt cttccctgaa gacattactg tggagtggca gtggatgg | 1140 |
| cagccagcgg agaactacaa gaacactcag cccatcatgg acacagatgg ctcttacttc | 1200 |
| atctacagca agctcaatgt gcagaagagc aactggggagg cagggaaatac tttcacctgc | 1260 |
| tctgtgttac atgagggcct gcacaaccac catactgaga agagcctctc ccactctcct | 1320 |
| ggtaaatga | 1329 |

<210> SEQ ID NO 362

<211> LENGTH: 461

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 362

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Trp | Ser | Ser | Ile | Ile | Leu | Phe | Leu | Val | Ala | Thr | Ala | Thr | Gly |
| 1 | | | | | 5 | | | | 10 | | | 15 | | | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | His | Ser | Gln | Val | Gln | Leu | Gln | Pro | Gly | Thr | Glu | Leu | Val | Arg |
| | | | | 20 | | | 25 | | | | 30 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Thr | Ser | Val | Lys | Leu | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Ile | Phe |
| | | | | 35 | | | 40 | | | | 45 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Thr | Tyr | Trp | Met | Asn | Trp | Val | Lys | Gln | Arg | Pro | Gly | Gln | Gly | Leu |
| | | | | 50 | | | 55 | | | 60 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Trp | Ile | Gly | Met | Ile | His | Pro | Ser | Ala | Ser | Glu | Ile | Arg | Leu | Asp |
| | | | | 65 | | | 70 | | | 75 | | | 80 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Lys | Phe | Lys | Asp | Lys | Ala | Thr | Leu | Thr | Leu | Asp | Lys | Ser | Ser | Ser |
| | | | | 85 | | | 90 | | | 95 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Tyr | Met | His | Leu | Ser | Gly | Pro | Thr | Ser | Val | Asp | Ser | Ala | Val |
| | | | | | 100 | | | 105 | | | 110 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Cys | Ala | Arg | Ser | Gly | Glu | Trp | Gly | Ser | Met | Asp | Tyr | Trp | Gly |
| | | | | 115 | | | 120 | | | 125 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Gly | Thr | Ser | Val | Thr | Val | Ser | Ser | Ala | Lys | Thr | Thr | Pro | Pro | Ser |
| | | | | 130 | | | 135 | | | 140 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Pro | Leu | Ala | Pro | Gly | Ser | Ala | Ala | Gln | Thr | Asn | Ser | Met | Val |
| | | | | 145 | | | 150 | | | 155 | | | 160 | | |

Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val

US 9,089,553 B2

367**368**

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| 165 | 170 | 175 |
|---|-----|-----|
| Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala | | |
| 180 | 185 | 190 |
| Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro | | |
| 195 | 200 | 205 |
| Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro | | |
| 210 | 215 | 220 |
| Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly | | |
| 225 | 230 | 235 |
| Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile | | |
| 245 | 250 | 255 |
| Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys | | |
| 260 | 265 | 270 |
| Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln | | |
| 275 | 280 | 285 |
| Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln | | |
| 290 | 295 | 300 |
| Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu | | |
| 305 | 310 | 315 |
| Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg | | |
| 325 | 330 | 335 |
| Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys | | |
| 340 | 345 | 350 |
| Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro | | |
| 355 | 360 | 365 |
| Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr | | |
| 370 | 375 | 380 |
| Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln | | |
| 385 | 390 | 395 |
| Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly | | |
| 405 | 410 | 415 |
| Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu | | |
| 420 | 425 | 430 |
| Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn | | |
| 435 | 440 | 445 |
| His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys | | |
| 450 | 455 | 460 |

<210> SEQ ID NO 363

<211> LENGTH: 1386

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 363

| | |
|---|-----|
| atgggatgga gctctatcat cctttcttg gtagcaacag ctacagggtgt ccactccag | 60 |
| gtccaaactac agcagcctgg gactgagctg gtgaggcctg gaacttcagt gaagttgtcc | 120 |
| tgtaaggctt ctggctacat cttcaccacc tactggatgaa actgggtgaa acagaggcct | 180 |
| ggacaaggcc ttgagtggat tggcatgatt catccttccg caagtgaaat taggttggat | 240 |
| cagaaaattca aggacaaggc cacattgact cttgacaaat cctccagcac agcctatatg | 300 |
| caccttcagcg gccccacatc tgtggattct gcgggtctatt actgtgcaag atcaggggaa | 360 |
| tgggggtcta tggactactg gggtaagga acctcagtca ccgtctccctc agccaaaacg | 420 |
| acaccccccata ctgtctatcc actggccctt ggatctgctg cccaaactaa ctccatggtg | 480 |

-continued

| | |
|---|------|
| accctggat gcctggtaa gggctatttc cctgagccag tgacagtgc ctgaaactct | 540 |
| ggatccctgt ccagcggtgt gcacaccttc ccagctgtcc tgcagtctga cctctacact | 600 |
| ctgagcagct cagtgactgt cccctccagc acctggccca gcgagaccgt cacctgcaac | 660 |
| gttgcaccacc cggccagcag cacaagggtg gacaagaaaa ttgtgcagg ggatttggt | 720 |
| tgtaaggcctt gcatatgtac agtcccagaa gtatcatctg tttcatctt ccccccaaag | 780 |
| cccaaggatg tgctcaccat tactctgact cctaaggtaa cgtgttgtgt ggttagacatc | 840 |
| agcaaggatg atcccgaggt ccagttcagc tggttttagt atgatgtgga ggtgcacaca | 900 |
| getcagacgc aaccccgaaa ggacgatcc aacagcactt tccgctcaat cagtgaactt | 960 |
| cccatcatgc accaggactg gctcaatggc aaggagttca aatgcagggt caacagtgc | 1020 |
| gtttccctg ccccccataa gaaaaccatc tccaaaacca aaggcagacc gaaggctcca | 1080 |
| caggtgtaca cccatccacc tcccaaggag cagatggccca aggataaaagt cagtctgacc | 1140 |
| tgcataataa cagacttctt cccctgaagac attactgtgg agtggcagtg gaatggcag | 1200 |
| ccagcggaga actacaagaa cactcagccc atcatggaca cagatggctc ttacttcattc | 1260 |
| taacagcaagc tcaatgtgca gaagagcaac tggaggcag gaaataactt cacctgctct | 1320 |
| gtgttacatg agggcctgca caaccaccat actgagaaga gctctccca ctctctgg | 1380 |
| aaatga | 1386 |

<210> SEQ ID NO 364

<211> LENGTH: 106

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 364

| | | | |
|---|---|----|----|
| Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly | | | |
| 1 | 5 | 10 | 15 |

| | | | |
|---|----|----|--|
| Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr | | | |
| 20 | 25 | 30 | |

| | | | |
|---|----|----|--|
| Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile | | | |
| 35 | 40 | 45 | |

| | | | |
|---|----|----|--|
| Tyr Ser Thr Ser Arg Leu Asn Ser Gly Val Pro Ser Arg Phe Ser Gly | | | |
| 50 | 55 | 60 | |

| | | | |
|---|----|----|----|
| Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro | | | |
| 65 | 70 | 75 | 80 |

| | | | |
|---|----|----|--|
| Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Ile Lys His Pro Thr | | | |
| 85 | 90 | 95 | |

| | | |
|---|-----|--|
| Phe Gly Gln Gly Thr Lys Val Glu Ile Lys | | |
| 100 | 105 | |

<210> SEQ ID NO 365

<211> LENGTH: 318

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 365

| | |
|---|-----|
| gacatccaga tgacccagtc tccatccctcc ctgtctgcat ctgttaggtga ccgtgtcacc | 60 |
| atcacttgcc ggcgaagtca ggatattagc agctatttaa attggatatca gcagaaacca | 120 |
| ggaaaagccc ctaagctct gatctattct acttcccggt tgaatagtgg ggtcccatca | 180 |
| cgcttcagtg gcagtggtc tggacagat ttcaactctca ccatcagcag tctgcaacct | 240 |
| gaagattttg caacttacta ctgtcaacag gatattaaac accctacgtt cggtcaaggc | 300 |

-continued

accaagggtgg agatcaaa

318

<210> SEQ ID NO 366
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 366

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Val | Gln | Ser | Gly | Ala | Glu | Val | Lys | Lys | Pro | Gly | Ser |
| 1 | | | | 5 | | | | | 10 | | | | 15 | | |
| Ser | Val | Lys | Val | Ser | Cys | Lys | Ala | Ser | Gly | Phe | Thr | Phe | Thr | Asp | Tyr |
| | 20 | | | | 25 | | | | | 30 | | | | | |
| Ile | Met | His | Trp | Val | Arg | Gln | Ala | Pro | Gly | Gln | Gly | Leu | Glu | Trp | Met |
| | 35 | | | | 40 | | | | | 45 | | | | | |
| Gly | Tyr | Ile | Asn | Pro | Tyr | Asn | Asp | Asp | Thr | Glu | Tyr | Asn | Glu | Lys | Phe |
| | 50 | | | | 55 | | | | 60 | | | | | | |
| Lys | Gly | Arg | Val | Thr | Ile | Thr | Ala | Asp | Lys | Ser | Thr | Ser | Thr | Ala | Tyr |
| | 65 | | | | 70 | | | | 75 | | | | 80 | | |
| Met | Glu | Leu | Ser | Ser | Leu | Arg | Ser | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys |
| | 85 | | | | 90 | | | | 95 | | | | | | |
| Ala | Arg | Ser | Ile | Tyr | Tyr | Tyr | Asp | Ala | Pro | Phe | Ala | Tyr | Trp | Gly | Gln |
| | 100 | | | | 105 | | | | 110 | | | | | | |
| Gly | Thr | Leu | Val | Thr | Val | Ser | Ser | | | | | | | | |
| | 115 | | | | 120 | | | | | | | | | | |

<210> SEQ ID NO 367
<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 367

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| gaggtgcagc | tgggtcagtc | tggggctgag | gtgaagaagc | ctgggtccctc | ggtaaggc | 60 |
| tccgtcaagg | tttctggttt | tactttacc | gactatatta | tgcactgggt | gcgtcaggcc | 120 |
| cctggtaa | ggcttgagt | gatgggctat | atcaaccctt | ataatgtat | caccgaatac | 180 |
| aacgagaagt | tcaaggcccg | tgtcacgatt | accggggaca | aatccacgag | cacagcctac | 240 |
| atggagctga | gcagectgcg | ctctgaggac | acggccgtgt | attactgtgc | gcgttcgatt | 300 |
| tattactacg | atgccccgtt | tgcttactgg | ggccaaggga | ctctggcac | cgtctctagt | 360 |

<210> SEQ ID NO 368
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 368

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Met | Thr | Gln | Ser | Pro | Ser | Ser | Leu | Ser | Ala | Ser | Val | Gly |
| 1 | | | | 5 | | | 10 | | | 15 | | | | | |
| Asp | Arg | Val | Thr | Ile | Thr | Cys | Lys | Ala | Ser | Gln | Asp | Val | Phe | Thr | Ala |
| | 20 | | | | 25 | | | | | 30 | | | | | |
| Val | Ala | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Lys | Ala | Pro | Lys | Leu | Leu | Ile |
| | 35 | | | | 40 | | | | | 45 | | | | | |
| Tyr | Trp | Ala | Ser | Thr | Arg | His | Thr | Gly | Val | Pro | Ser | Arg | Phe | Ser | Gly |
| | 50 | | | | 55 | | | | 60 | | | | | | |
| Ser | Gly | Ser | Gly | Thr | Asp | Phe | Thr | Leu | Thr | Ile | Ser | Ser | Leu | Gln | Pro |
| | 65 | | | | 70 | | | | 75 | | | | 80 | | |
| Glu | Asp | Phe | Ala | Thr | Tyr | Tyr | Cys | Gln | Gln | Tyr | Ser | Ser | Tyr | Pro | Leu |

-continued

| | | |
|----|----|----|
| 85 | 90 | 95 |
|----|----|----|

| | | |
|---|-----|-----|
| Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg | 100 | 105 |
|---|-----|-----|

<210> SEQ ID NO 369

<211> LENGTH: 324

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 369

| | |
|--|-----|
| gatataccaga tgaccaggag cccgaggcgc ctgaggcgca gctgtggcga tcgcgtgacc | 60 |
| attacctgc aaggcgacca ggtatgttt accgcggtgg cgtggtatca gcagaaaccg | 120 |
| ggcaaaggcg cggaaactgct gatttattgg gcgagcaccc gccataccgg cgtgcggagt | 180 |
| cgcgttagcg gcagcggcag cggcaccat tttaccctga ccattagcag cctgcagccg | 240 |
| gaagattttg cgacctatta ttgccagcag tatagcagct atccgctgac ctttggccgc | 300 |
| ggcaccaaaag tggaaaattaa acgt | 324 |

<210> SEQ ID NO 370

<211> LENGTH: 119

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 370

| | | | |
|---|-----|-----|----|
| Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala | | | |
| 1 | 5 | 10 | 15 |
| Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr | | | |
| 20 | 25 | 30 | |
| Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile | | | |
| 35 | 40 | 45 | |
| Gly Arg Ile Asp Pro Glu Asn Gly Asp Ile Ile Tyr Asp Pro Lys Phe | | | |
| 50 | 55 | 60 | |
| Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr | | | |
| 65 | 70 | 75 | 80 |
| Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys | | | |
| 85 | 90 | 95 | |
| Ala Tyr Asp Ala Gly Asp Pro Ala Trp Phe Thr Tyr Trp Gly Gln Gly | | | |
| 100 | 105 | 110 | |
| Thr Leu Val Thr Val Ser Ser | | | |
| 115 | | | |

<210> SEQ ID NO 371

<211> LENGTH: 357

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 371

| | |
|---|-----|
| gaagtgcagc tggtgccagag cggcgccgaa gtaaaaaac cgggcgcgag cgtgaaagt | 60 |
| agctgcaaag cgagcggtt taacattaaa gattattata tgcattgggt gcgcaggcg | 120 |
| cggggccagg gcctggatg gatggccgc attgatccgg aaaacggcga tattattat | 180 |
| gatccgaaat ttcaggccc cgtgaccatg accaccgata ccagcaccag caccgcgtat | 240 |
| atggaaactgc gcagcctgcg cagcgatgtat accgcggtgtt attattgcgc gtatgtgcg | 300 |
| ggcgatccgg cgtggtttac ctattgggc cagggcaccc tggtgaccgt ctgcgac | 357 |

<210> SEQ ID NO 372

US 9,089,553 B2

375**376**

-continued

<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 372

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Gln | Leu | Thr | Gln | Ser | Pro | Ser | Phe | Leu | Ser | Ala | Ser | Val | Gly |
| 1 | | | | | | | 5 | | 10 | | | | | 15 | |

Asp Arg Val Thr Ile Thr Cys Ser Val Ser Ser Ser Ile Ser Ser Ser

| | | | | | | | | | | | | | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|--|
| 20 | | | | | | | 25 | | | | | 30 | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|--|

Asn Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu

| | | | | | | | | | | | | | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|--|
| 35 | | | | | | | 40 | | | | | 45 | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|--|

Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser

| | | | | | | | | | | | | | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|--|
| 50 | | | | | | | 55 | | | | | 60 | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|--|

Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln

| | | | | | | | | | | | | | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|----|
| 65 | | | | | | | 70 | | | | | 75 | | | 80 |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|----|

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Thr Thr Tyr

| | | | | | | | | | | | | | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|--|
| 85 | | | | | | | 90 | | | | | 95 | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|--|

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg

| | | | | | | | | | | | | | | | |
|-----|--|--|--|--|--|--|-----|--|--|--|--|--|--|--|--|
| 100 | | | | | | | 105 | | | | | | | | |
|-----|--|--|--|--|--|--|-----|--|--|--|--|--|--|--|--|

<210> SEQ ID NO 373
<211> LENGTH: 324
<212> TYPE: DNA
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 373

| | | | | | | |
|-------------|------------|------------|-------------|------------|------------|-----|
| gatattcagc | tgacccagag | cccgagcttt | ctgagcgcga | gcgtgggcga | tcgcgtgacc | 60 |
| attacctgca | gcgtgagcag | cagcattagc | agcagcaacc | tgcattggta | tcagcagaaa | 120 |
| ccggggcaaag | cggccaaact | gctgatttat | ggcacccagca | acctggcgag | cggcgtgccg | 180 |
| agccgcctta | gcggcagcgg | cageggcacc | gaatttaccc | tgaccattag | cagcctgcag | 240 |
| ccggaaagatt | ttgcgcacta | ttattgccag | cagtggacca | ccacctatac | ctttggccag | 300 |
| ggcacccaaac | tggaaattaa | acgt | | | | 324 |

<210> SEQ ID NO 374
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 374

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Gln | Leu | Val | Gln | Ser | Gly | Ala | Glu | Val | Lys | Lys | Pro | Gly | Ala |
| 1 | | | | | | | | | 5 | | 10 | | | 15 | |

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr

| | | | | | | | | | | | | | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|--|
| 20 | | | | | | | 25 | | | | | 30 | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|--|

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met

| | | | | | | | | | | | | | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|--|
| 35 | | | | | | | 40 | | | | | 45 | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|--|

Gly Arg Ile Asp Pro Asp Asn Gly Glu Ser Thr Tyr Val Pro Lys Phe

| | | | | | | | | | | | | | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|--|
| 50 | | | | | | | 55 | | | | | 60 | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|--|

Gln Gly Arg Val Thr Met Thr Asp Thr Ser Thr Ser Thr Ala Tyr

| | | | | | | | | | | | | | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|----|
| 65 | | | | | | | 70 | | | | | 75 | | | 80 |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|----|

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys

| | | | | | | | | | | | | | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|--|
| 85 | | | | | | | 90 | | | | | 95 | | | |
|----|--|--|--|--|--|--|----|--|--|--|--|----|--|--|--|

Ala Arg Glu Gly Leu Asp Tyr Gly Asp Tyr Tyr Ala Val Asp Tyr Trp

| | | | | | | | | | | | | | | | |
|-----|--|--|--|--|--|--|-----|--|--|--|--|-----|--|--|--|
| 100 | | | | | | | 105 | | | | | 110 | | | |
|-----|--|--|--|--|--|--|-----|--|--|--|--|-----|--|--|--|

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

| | | | | | | | | | | | | | | | |
|-----|--|--|--|--|--|--|-----|--|--|--|--|--|--|--|--|
| 115 | | | | | | | 120 | | | | | | | | |
|-----|--|--|--|--|--|--|-----|--|--|--|--|--|--|--|--|

-continued

<210> SEQ ID NO 375
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 375

```
gaagtgcagc tgggtgcagag cggcgccgaa gtgaaaaaac cgggcgcgag cgtgaaagtg      60
agctgcggaa cggccggctt taacattaaa gattattata ttcatgggt ggcgcaggcg      120
ccggggccagg gcctggaatg gatggggccgc attgatccgg ataacggcga aagcacctat      180
gtgcccggaaat ttcatggccg cgtgaccatg accaccgata ccagcaccag caccgcgtat      240
atggaaactgc gcagcctgcg cagcgatgtat accgcgggtgt attattgcgc ggcgcgaaggc      300
ctggattatg gcgattatta tgccgtggat tattggggcc agggcacctt ggtgaccgtc      360
tcgagc                                              366
```

<210> SEQ ID NO 376
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 376

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1           5          10          15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20          25          30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35          40          45
Tyr Tyr Thr Ser Arg Leu Leu Ser Gly Val Pro Ser Arg Phe Ser Gly
50          55          60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65          70          75          80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Thr Leu Pro Tyr
85          90          95
Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
100         105
```

<210> SEQ ID NO 377
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 377

```
gacatccaga tgacctcagtc tccatccctcc ctctccgcgtt ccgttaggcga ccgcgttaacc      60
ataacatgtt gaggcatctca agatatttcc aactatttga attgggtacca aaaaaaccc      120
ggccaaaggac cttaaactcctt cattttactat acatcaagac ttctctccgg cggtttccatca      180
cgattctcgat gtcggcgctc cggcacagat ttcacactca ctatccctc cctccaacca      240
gaagattttg caaccttata ctgtcaacaa ggcgatacac tccctatacac attcggccgc      300
ggcacaaaag ttgaaattaa a                                              321
```

<210> SEQ ID NO 378
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 378

US 9,089,553 B2

379**380**

-continued

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30

Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val
 100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> SEQ ID NO 379

<211> LENGTH: 369

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 379

```

gaggtgcagc tggtgccagag cggcgccgag gtaaaaaaac caggagcaag cgtaaaagtt      60
tcttgtaaag caagcgata tacattaca gattacaaca tgcattgggt aagacaagcg      120
ccaggacaag gattgaatg gatgggcgaa attaacccta atagtggagg agcaggctac      180
aatcaaaaat tcaaaggag agttacaatg acaacagaca caagcacttc aacagcatat      240
atggaaactgc gatcaattag aagcgacgat acagctgtat actattgcgc acgacttggg      300
tatgatgata tatatgatga ctggtatttc gatgtttggg gccagggAAC aacagttacc      360
gtctctagt                                         369

```

<210> SEQ ID NO 380

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 380

Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Thr Ser Ser
 20 25 30

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
 35 40 45

Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
 65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Phe Phe Pro
 85 90 95

Ser Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> SEQ ID NO 381

<211> LENGTH: 324

<212> TYPE: DNA

-continued

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 381

| | | | | |
|----------------------------------|------------|------------------------|-----------------------|-----|
| gacateccagc tgaccaggag ccccagctc | cttccgcac | ccgttgtga ccgagtaaca | 60 | |
| atcacatgcc gcgcctcatc | ttagttaca | tcttcttatac ttaattggta | tcaacaaaaa | 120 |
| ccaggaaaag cacctaaact | tcttatatac | tctacatcta atctcgatc | aggagttccc | 180 |
| tctcgatttt caggatctgg | atcaggcaca | gaatttacac ttactatatac | atcaactccaa | 240 |
| ccagaagact tcgcccactta | ttactgccaa | caatacgtt | tttttccaag cacattcgga | 300 |
| ggaggtacaa aagttagaaat | caag | | | 324 |

<210> SEQ ID NO 382

<211> LENGTH: 121

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 382

| | | | |
|---|-----|-----|----|
| Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala | | | |
| 1 | 5 | 10 | 15 |
| Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr | | | |
| 20 | 25 | 30 | |
| Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met | | | |
| 35 | 40 | 45 | |
| Gly Asp Ile Asn Pro Tyr Asn Asp Asp Thr Thr Tyr Asn His Lys Phe | | | |
| 50 | 55 | 60 | |
| Lys Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr | | | |
| 65 | 70 | 75 | 80 |
| Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys | | | |
| 85 | 90 | 95 | |
| Ala Arg Glu Thr Ala Val Ile Thr Thr Asn Ala Met Asp Tyr Trp Gly | | | |
| 100 | 105 | 110 | |
| Gln Gly Thr Thr Val Thr Val Ser Ser | | | |
| 115 | 120 | | |

<210> SEQ ID NO 383

<211> LENGTH: 363

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 383

| | | | |
|-----------------------------------|-----------------------|-----------------------|-----|
| gaggtgcagc tggcagag cggcgccag | gtcaagaaac ctggagcaag | cgtaaaggtt | 60 |
| agttgcaaag catctggata cacatttacc | gactactaca | tgaattgggt acgacaagcc | 120 |
| cctggacaaa gacttgaatg gatgggagac | attaaccctt | ataacgacga cactacatac | 180 |
| aatcataaat ttaaaggaag agttacaatt | acaagagata | catccgatc aaccgcctat | 240 |
| atggaaacttt octcattgag atctgaagac | actgctgttt | attactgtgc aagagaaact | 300 |
| gccgttatta ctactaacgc tatggattac | tgggtcaag | gaaccactgt taccgtctct | 360 |
| agt | | | 363 |

<210> SEQ ID NO 384

<211> LENGTH: 108

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 384

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

-continued

| | | | |
|---|-----|----|----|
| 1 | 5 | 10 | 15 |
| Asp Arg Val Thr Ile Thr Cys Ser Val Ser Ser Thr Ile Ser Ser Asn | | | |
| 20 | 25 | 30 | |
| His Leu His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu | | | |
| 35 | 40 | 45 | |
| Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser | | | |
| 50 | 55 | 60 | |
| Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln | | | |
| 65 | 70 | 75 | 80 |
| Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Tyr Pro | | | |
| 85 | 90 | 95 | |
| Leu Thr Phe Gly Gly Thr Lys Val Glu Ile Lys | | | |
| 100 | 105 | | |

<210> SEQ ID NO 385

<211> LENGTH: 324

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 385

| | |
|--|-----|
| gacatccaga tgaccaggc tccatccctcc ctctcagcat ccgttaggcga tagagttaca | 60 |
| ataacatgcg gcgtatcatc aactatatac tcaaattatc ttcatgggtt ccaacagaaa | 120 |
| ccccggcaaa ag cacctaaatc acttatatac ggcacatcaa atctcgcatc aggcgttcct | 180 |
| tcaagatttt caggctctgg ctcaggcacc gactttactc ttacaatatc ctccctccaa | 240 |
| cccgaaagact tcgcaaccta ttactgtcaa caatggcct catatccact cacatttggc | 300 |
| ggcggcacaa aagttagaaat taaa | 324 |

<210> SEQ ID NO 386

<211> LENGTH: 125

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 386

| | | | |
|---|-----|-----|----|
| Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala | | | |
| 1 | 5 | 10 | 15 |
| Ser Val Lys Val Ser Cys Lys Ala Ser Asp Phe Asn Ile Lys Asp Phe | | | |
| 20 | 25 | 30 | |
| Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile | | | |
| 35 | 40 | 45 | |
| Gly Arg Ile Asp Pro Glu Asn Gly Asp Thr Leu Tyr Asp Pro Lys Phe | | | |
| 50 | 55 | 60 | |
| Gln Asp Lys Val Thr Met Thr Asp Thr Ser Thr Ser Ala Tyr | | | |
| 65 | 70 | 75 | 80 |
| Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys | | | |
| 85 | 90 | 95 | |
| Ala Arg Glu Ala Asp Tyr Phe His Asp Gly Thr Ser Tyr Trp Tyr Phe | | | |
| 100 | 105 | 110 | |
| Asp Val Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser | | | |
| 115 | 120 | 125 | |

<210> SEQ ID NO 387

<211> LENGTH: 375

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 387

-continued

| | |
|---|-----|
| gagggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcc tc agtgaagg tc | 60 |
| tccctgcaagg cttctgactt caacattaaa gacttctatc tacactgggt gcgacagg cc | 120 |
| cctggacaag ggcttgagt gatttggagg attgatcctg agaatggta tactttat | 180 |
| gaccgcagaat tccaggacaa ggtcaccatg accacagaca cgtccaccag cacagcctac | 240 |
| atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagagg cg | 300 |
| gattatttcc acgatggta ctcctactgg tacttcgatg tctggggccg tggcaccc tg | 360 |
| gtcaccgtct ctatg | 375 |

<210> SEQ ID NO 388

<211> LENGTH: 106

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 388

| | | | |
|---|---|----|----|
| Asp Ile Gln Leu Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly | | | |
| 1 | 5 | 10 | 15 |

| | | | |
|---|----|----|--|
| Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Ile Ser Tyr Ile | | | |
| 20 | 25 | 30 | |

| | | | |
|---|----|----|--|
| His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr | | | |
| 35 | 40 | 45 | |

| | | | |
|---|----|----|--|
| Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser | | | |
| 50 | 55 | 60 | |

| | | | |
|---|----|----|----|
| Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu | | | |
| 65 | 70 | 75 | 80 |

| | | | |
|---|----|----|--|
| Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asp Pro Leu Thr | | | |
| 85 | 90 | 95 | |

| | | |
|---|-----|--|
| Phe Gly Gly Gly Thr Lys Val Glu Ile Lys | | |
| 100 | 105 | |

<210> SEQ ID NO 389

<211> LENGTH: 318

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 389

| | |
|--|-----|
| gacatccagt tgacctcagtc tccatccttc ctgtctgcat ctgttaggaga cagagtacc | 60 |
| atcacttgca gggccagtc aagtataagt tacatacact ggtatcagca aaaaccagg | 120 |
| aaagcccccta agctcctgat ctatgccaca tccaacctgg cttctggggt cccatcaagg | 180 |
| ttcagcggca gtggatctgg gacagaattc actctcacaa tcagcagcct gcagectgaa | 240 |
| gattttgcaa cttattactg tcagcagtcg agtagtgacc cactcacgtt cggcggagg | 300 |
| accaagggtgg agatcaaa | 318 |

<210> SEQ ID NO 390

<211> LENGTH: 121

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 390

| | | | |
|---|---|----|----|
| Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala | | | |
| 1 | 5 | 10 | 15 |

| | | | |
|---|----|----|--|
| Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asp Ile Lys Asp Tyr | | | |
| 20 | 25 | 30 | |

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile

-continued

35 40 45

Gly Arg Val Asp Pro Asp Asn Gly Glu Thr Glu Phe Ala Pro Lys Phe
50 55 60

Pro Gly Lys Val Thr Met Thr Thr Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Tyr Asp Gly Thr Tyr Thr Trp Phe Pro Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 391

<211> LENGTH: 363

<212> TYPE: DNA

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 391

| | |
|--|-----|
| gaggtgcagc tggtgcaagtc tggggcttagt gtgaagaagc ctggggccctc agtgaaggtc | 60 |
| tccatcgaaagg cttctggatt cgacattaag gactactata tacactgggt gcgacaggcc | 120 |
| cctggacaag ggcttgagtg gatcggaagg gttgatectg acaatggtga gactgaattt | 180 |
| gccccgaagt tcccgccaa ggtcaccatcg accacagaca cgtccatcag cacagcctac | 240 |
| atggagctga gcaggcttagt atctgacgac acggccgtgt attactgtgc gagagaagac | 300 |
| tacgatggta octcacacctg gttcccttat tggggccaag ggactctggt caccgtctct | 360 |
| agt | 363 |

<210> SEQ ID NO 392

<211> LENGTH: 448

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 392

| | |
|---|--|
| Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala | |
| 1 5 10 15 | |

| | |
|---|--|
| Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr | |
| 20 25 30 | |

| | |
|---|--|
| Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met | |
| 35 40 45 | |

| | |
|---|--|
| Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe | |
| 50 55 60 | |

| | |
|---|--|
| Lys Gly Arg Val Thr Met Thr Asp Thr Ser Thr Ser Thr Ala Tyr | |
| 65 70 75 80 | |

| | |
|---|--|
| Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys | |
| 85 90 95 | |

| | |
|---|--|
| Ala Arg Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val | |
| 100 105 110 | |

| | |
|---|--|
| Trp Gly Gln Gly Thr Thr Val Thr Ser Ser Ala Ser Thr Lys Gly | |
| 115 120 125 | |

| | |
|---|--|
| Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser | |
| 130 135 140 | |

US 9,089,553 B2

389**390**

-continued

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 180 185 190
 Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
 195 200 205
 Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
 210 215 220
 Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
 225 230 235 240
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 245 250 255
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270
 Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
 290 295 300
 Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320
 Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
 325 330 335
 Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 340 345 350
 Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
 385 390 395 400
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

```

<210> SEQ ID NO 393
<211> LENGTH: 446
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<223> OTHER INFORMATION: Humanized Antibody Sequence

```

<400> SEQUENCE: 393

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30
 Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
 35 40 45

US 9,089,553 B2

391**392**

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Gly Asp Ile Asn Pro Tyr Asn Asp Asp Thr Thr Tyr Asn His Lys Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Thr Ala Val Ile Thr Thr Asn Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
210 215 220

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
290 295 300

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
325 330 335

Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

<210> SEQ_ID NO 394

<211> LENGTH: 450

<212> TYPE: PRT

-continued

<213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic Polypeptide
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <223> OTHER INFORMATION: Humanized Antibody Sequence

 <400> SEQUENCE: 394

 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

 Ser Val Lys Val Ser Cys Lys Ala Ser Asp Phe Asn Ile Lys Asp Phe
 20 25 30

 Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

 Gly Arg Ile Asp Pro Glu Asn Gly Asp Thr Leu Tyr Asp Pro Lys Phe
 50 55 60

 Gln Asp Lys Val Thr Met Thr Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

 Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

 Ala Arg Glu Ala Asp Tyr Phe His Asp Gly Thr Ser Tyr Trp Tyr Phe
 100 105 110

 Asp Val Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
 115 120 125

 Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
 130 135 140

 Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
 145 150 155 160

 Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
 165 170 175

 Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
 180 185 190

 Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
 195 200 205

 Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
 210 215 220

 Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
 225 230 235 240

 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 245 250 255

 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 260 265 270

 Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 275 280 285

 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
 290 295 300

 Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
 305 310 315 320

 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
 325 330 335

 Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350

 Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365

 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

-continued

370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445

Pro Gly
 450

<210> SEQ ID NO 395

<211> LENGTH: 446

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 395

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asp Ile Lys Asp Tyr
 20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Arg Val Asp Pro Asp Asn Gly Glu Thr Glu Phe Ala Pro Lys Phe
 50 55 60

Pro Gly Lys Val Thr Met Thr Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Asp Tyr Asp Gly Thr Tyr Thr Trp Phe Pro Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
 130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
 210 215 220

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
 225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255

Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp Pro Glu

-continued

260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
290 295 300

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
325 330 335

Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

<210> SEQ_ID NO 396

<211> LENGTH: 445

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic Polypeptide

<220> FEATURE:

<221> NAME/KEY: MISC_FEATURE

<223> OTHER INFORMATION: Humanized Antibody Sequence

<400> SEQUENCE: 396

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr Asp Tyr
20 25 30

Ile Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Asp Thr Glu Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ile Tyr Tyr Asp Ala Pro Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val

-continued

| 165 | 170 | 175 |
|---|-----|-----|
| Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro | | |
| 180 | 185 | 190 |
| Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys | | |
| 195 | 200 | 205 |
| Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val | | |
| 210 | 215 | 220 |
| Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe | | |
| 225 | 230 | 235 |
| Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro | | |
| 245 | 250 | 255 |
| Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val | | |
| 260 | 265 | 270 |
| Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr | | |
| 275 | 280 | 285 |
| Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val | | |
| 290 | 295 | 300 |
| Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys | | |
| 305 | 310 | 315 |
| Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser | | |
| 325 | 330 | 335 |
| Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro | | |
| 340 | 345 | 350 |
| Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val | | |
| 355 | 360 | 365 |
| Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly | | |
| 370 | 375 | 380 |
| Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp | | |
| 385 | 390 | 395 |
| Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp | | |
| 405 | 410 | 415 |
| Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His | | |
| 420 | 425 | 430 |
| Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly | | |
| 435 | 440 | 445 |

What is claimed is:

1. A method for inhibiting bone resorption in a human, the method comprising administering to the human an amount from about 1 mg/kg to about 8 mg/kg of an antibody or fragment thereof that (i) demonstrates a binding affinity for sclerostin of SEQ ID NO: 1 of less than or equal to 1×10^{-9} M and (ii) comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 378 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 376, wherein bone resorption is inhibited.
2. The method of claim 1, wherein the antibody comprises heavy chains comprising the amino acid sequence of SEQ ID NO: 145 or 392 and light chains comprising the amino acid sequence of SEQ ID NO: 141.
3. The method of claim 1, wherein the amount of antibody or fragment thereof does not result in hypocalcemia or hypercalcemia.
4. The method of claim 1, wherein an amount of antibody or fragment thereof is administered to the human once every two weeks.
5. The method of claim 1, wherein an amount of antibody or fragment thereof administered to the human once a month.

6. The method of claim 1, wherein the antibody or fragment thereof is a monoclonal antibody.

7. The method of claim 6, wherein the antibody or fragment thereof is a humanized antibody or a chimeric antibody.

8. The method of claim 1, wherein the antibody or fragment thereof is a humanized antibody or a chimeric antibody.

9. A method for increasing bone mineral density in a human, the method comprising administering to the human an antibody or fragment thereof in an amount from about 1 mg/kg to about 8 mg/kg, wherein the antibody or fragment thereof (i) demonstrates a binding affinity for sclerostin of SEQ ID NO: 1 of less than or equal to 1×10^{-9} M and (ii) comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 378 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 376, and wherein bone mineral density is increased.

10. The method of claim 9, wherein hip, spine, wrist, finger, shin bone and/or heel bone mineral density is increased by at least about 1%.

11. The method of claim 10, wherein bone mineral density in the spine is increased by at least about 1%.

401

12. The method of claim 9, wherein bone mineral density is increased to the range of about 1 to 2.5 standard deviations below the normal bone mineral density of a healthy young adult.

13. The method of claim 9, wherein bone mineral density is increased to the range of about 0 to 1 standard deviations below the normal bone mineral density of a healthy young adult.

14. The method of claim 9, wherein an amount of antibody or fragment thereof is administered to the human once every two weeks.

15. The method of claim 9, wherein an amount of antibody or fragment thereof is administered to the human once a month.

16. The method of claim 9, wherein the antibody comprises heavy chains comprising the amino acid sequence of SEQ ID NO: 145 or 392 and light chains comprising the amino acid sequence of SEQ ID NO: 141.

17. The method of claim 9, comprising administering to said human from about 1 mg/kg to about 3 mg/kg of the antibody or fragment thereof.

18. The method of claim 9, wherein the antibody or fragment thereof is a monoclonal antibody.

19. The method of claim 18, wherein the antibody or fragment thereof is a humanized antibody or a chimeric antibody.

20. The method of claim 9, wherein the antibody is a humanized antibody or a chimeric antibody.

21. A method for treating a bone-related disorder in a human, the method comprising

(a) administering to the human an antibody or fragment thereof in an amount from about 1 mg/kg to about 8 mg/kg for a first period of time, wherein the amount is effective to increase bone mineral density at the hip, spine, wrist, finger, shin bone and/or heel by at least about 3%, and

(b) administering to the human an antibody or fragment thereof in an amount of from about 1 mg/kg to about 8 mg/kg for a second period of time effective to maintain bone mineral density,

wherein the antibody or fragment thereof (i) demonstrates a binding affinity for sclerostin of SEQ ID NO: 1 of less than or equal to 1×10^{-9} M and (ii) comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 378 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 376.

22. The method of claim 21, wherein the first period of time is 3 months or less.

23. The method of claim 21, wherein the second period of time is at least 6 months.

24. The method of claim 21, wherein bone mineral density in the spine is increased by at least about 3%.

25. The method of claim 21, wherein an amount of antibody or fragment thereof is administered to the human once every two weeks.

26. The method of claim 21, wherein an amount of antibody or fragment thereof is administered to the human once a month.

27. The method of claim 21 in which the bone-related disorder is selected from the group consisting of achondroplasia, cleidocranial dysostosis, enchondromatosis, fibrous dysplasia, Gaucher's Disease, hypophosphatemic rickets, Marfan's syndrome, multiple hereditary exostoses, neurofibromatosis, osteogenesis imperfecta, osteopetrosis, osteopoikilosis, sclerotic lesions, pseudoarthrosis, pyogenic osteomyelitis, periodontal disease, anti-epileptic drug induced bone loss, primary and secondary hyperparathyroid-

402

ism, familial hyperparathyroidism syndromes, weightlessness induced bone loss, osteoporosis in men, postmenopausal bone loss, osteoarthritis, renal osteodystrophy, infiltrative disorders of bone, oral bone loss, osteonecrosis of the jaw, juvenile Paget's disease, melorheostosis, metabolic bone diseases, mastocytosis, sickle cell anemia/disease, organ transplant related bone loss, kidney transplant related bone loss, systemic lupus erythematosus, ankylosing spondylitis, epilepsy, juvenile arthritides, thalassemia, mucopolysaccharidoses, Fabry Disease, Turner Syndrome, Down Syndrome, Klinefelter Syndrome, leprosy, Perthes' Disease, adolescent idiopathic scoliosis, infantile onset multi-system inflammatory disease, Winchester Syndrome, Menkes Disease, Wilson's Disease, ischemic bone disease, Legg-Calve-Perthes disease, regional migratory osteoporosis, anemic states, conditions caused by steroids, glucocorticoid-induced bone loss, heparin-induced bone loss, bone marrow disorders, scurvy, malnutrition, calcium deficiency, osteoporosis, osteopenia, alcoholism, chronic liver disease, postmenopausal state, chronic inflammatory conditions, rheumatoid arthritis, inflammatory bowel disease, ulcerative colitis, inflammatory colitis, Crohn's disease, oligomenorrhea, amenorrhea, pregnancy, diabetes mellitus, hyperthyroidism, thyroid disorders, parathyroid disorders, Cushing's disease, acromegaly, hypogonadism, immobilization or disuse, reflex sympathetic dystrophy syndrome, regional osteoporosis, osteomalacia, bone loss associated with joint replacement, HIV associated bone loss, bone loss associated with loss of growth hormone, bone loss associated with cystic fibrosis, chemotherapy associated bone loss, tumor induced bone loss, cancer-related bone loss, hormone ablative bone loss, multiple myeloma, drug-induced bone loss, anorexia nervosa, disease associated facial bone loss, disease associated cranial bone loss, disease associated bone loss of the jaw, disease associated bone loss of the skull, bone loss associated with aging, facial bone loss associated with aging, cranial bone loss associated with aging, jaw bone loss associated with aging, skull bone loss associated with aging, and bone loss associated with space travel.

28. The method of claim 21, wherein the antibody comprises heavy chains comprising the amino acid sequence of SEQ ID NO: 145 or 392 and light chains comprising the amino acid sequence of SEQ ID NO: 141.

29. The method of claim 21, wherein the antibody or fragment thereof is a monoclonal antibody.

30. The method of claim 29, wherein the antibody or fragment thereof is a humanized antibody or chimeric antibody.

31. The method of claim 21, wherein the antibody is a humanized antibody or a chimeric antibody.

32. A method of treating a bone-related disorder in a human suffering from or at risk of hypocalcemia or hypercalcemia, the method comprising administering to the human an antibody or fragment thereof in a therapeutically effective amount from about 1 mg/kg to about 8 mg/kg, wherein the antibody or fragment thereof (i) demonstrates a binding affinity for sclerostin of SEQ ID NO: 1 of less than or equal to 1×10^{-9} M and (ii) comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 378 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 376.

33. The method of claim 32, wherein the hypocalcemia or hypercalcemia results from chronic kidney disease, renal failure, primary or secondary hyperparathyroidism, pseudohyperparathyroidism, hypoparathyroidism, pseudohypoparathyroidism, magnesium depletion, severe hypermagnesemia, vitamin D deficiency, hyperphosphatemia, acute pancreatitis, hungry bone syndrome, chela-

403

tion, osteoblastic metastases, sepsis, surgery, chemotherapy, neoplasia syndrome, hypoparathyroidism, familial hypocalciuric hypercalcemia, sarcoidosis, tuberculosis, berylliosis, histoplasmosis, Candidiasis, Coccidioidomycosis, histiocytosis X, Hodgkin's or Non-Hodgkin's lymphoma, Crohn's disease, Wegener's granulomatosis, pneumonia, silicone-induced granulomas, administration of thiazide diuretics or lithium, or immobilization.

34. A method of treating a bone-related disorder in (a) a human in which treatment with a parathyroid hormone or analog thereof is contraindicated or (b) a human in which treatment with bisphosphonate is contraindicated, the method comprising administering to the human a therapeutically effective amount of an antibody or fragment thereof from about 1 mg/kg to about 8 mg/kg, wherein the antibody or fragment thereof (i) demonstrates a binding affinity for sclerostin of SEQ ID NO: 1 of less than or equal to 1×10^{-9} M and (ii) comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 378 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 376.

35. The method of claim 1, wherein the antibody or fragment thereof is administered to said human in an amount from about 70 mg to about 450 mg.

36. The method of claim 1, wherein the human is a postmenopausal woman.

37. The method of claim 36, wherein the antibody or fragment thereof is administered to said human in an amount from about 70 mg to about 450 mg.

38. The method of claim 9, wherein the antibody or fragment thereof is administered at about 2 mg/kg.

39. The method of claim 38, wherein the antibody or fragment thereof is administered once every two weeks.

40. The method of claim 38, wherein the antibody or fragment thereof is administered once per month.

41. The method of claim 21, wherein the antibody or fragment thereof is administered at about 2 mg/kg.

42. The method of claim 41, wherein the antibody or fragment thereof is administered once every two weeks.

43. The method of claim 41, wherein the antibody or fragment thereof is administered once per month.

44. The method of claim 9, wherein the human is a postmenopausal woman.

45. The method of claim 44, wherein the antibody or fragment thereof is administered to said human in an amount from about 70 mg to about 450 mg.

46. The method of claim 9, wherein the human is suffering from osteoporosis.

404

47. The method of claim 46, wherein the antibody or fragment thereof is administered to said human in an amount from about 70 mg to about 450 mg.

48. The method of claim 9, wherein the antibody or fragment thereof is administered to said human in an amount from about 70 mg to about 450 mg.

49. The method of claim 48, wherein the amount of antibody or fragment thereof administered to said human is about 70 mg.

50. The method of claim 48, wherein the amount of antibody or fragment thereof administered to said human is about 140 mg.

51. The method of claim 48, wherein the amount of antibody or fragment thereof administered to said human is about 210 mg.

52. The method of claim 21, wherein the human is a postmenopausal woman.

53. The method of claim 52, wherein the antibody or fragment thereof is administered to said human in an amount from about 70 mg to about 450 mg.

54. The method of claim 21, wherein the human is suffering from osteoporosis.

55. The method of claim 54, wherein the antibody or fragment thereof is administered to said human in an amount from about 70 mg to about 450 mg.

56. The method of claim 32, wherein the antibody comprises heavy chains comprising the amino acid sequence of SEQ ID NO: 145 or 392 and light chains comprising the amino acid sequence of SEQ ID NO: 141.

57. The method of claim 34, wherein the antibody comprises heavy chains comprising the amino acid sequence of SEQ ID NO: 145 or 392 and light chains comprising the amino acid sequence of SEQ ID NO: 141.

58. The method of claim 1, wherein the antibody or fragment thereof is a human antibody.

59. The method of claim 9, wherein the antibody or fragment thereof is a human antibody.

60. The method of claim 21, wherein the antibody or fragment thereof is a human antibody.

61. The method of claim 37, wherein the antibody or fragment thereof is a monoclonal antibody.

62. The method of claim 47, wherein the antibody or fragment thereof is a monoclonal antibody.

63. The method of claim 53, wherein the antibody or fragment thereof is a monoclonal antibody.

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